

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: October 13, 2006, 01:10:07 ; Search time 200 Seconds
(without alignments)
16.003 Million cell updates/sec

Title: US-10-537-648-1

Perfect score: 7

Sequence: 1 YLTQPS 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2589679 seqs, 457216429 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2546695

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : A_Geneseq_8.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2002s.*
- 6: Geneseq2003as.*
- 7: Geneseq2003bs.*
- 8: Geneseq2004s.*
- 9: Geneseq2005s.*
- 10: Geneseq2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	7	8	ADQ16409 Amino aci
2	6	85.7	371	7	ADF04626 Bacterial
3	6	85.7	415	6	ADB08414 Alloiooc
4	6	85.7	503	6	ADB08416 Alloiooc
5	6	85.7	717	6	ADB08418 Alloiooc
6	6	85.7	1526	4	ABB63939 Drosophil
7	5	71.4	8	2	RAW57619 T-cell re
8	5	71.4	8	3	RAY88609 T-cell re
9	5	71.4	10	2	AAW25909 Beta-2-mi
10	5	71.4	10	4	AAU25775 Breast ca
11	5	71.4	21	9	ADU98146 mSlo1 cal
12	5	71.4	22	4	RAM17466 Peptide #
13	5	71.4	22	4	ABB36486 Peptide #
14	5	71.4	22	4	AAW29985 Peptide #
15	5	71.4	22	4	ABB31280 Peptide #
16	5	71.4	22	4	ABB21828 Protein #
17	5	71.4	22	4	AAW69651 Human bon
18	5	71.4	22	4	AAW57249 Human bra
19	5	71.4	22	4	ABG51333 Human liv
20	5	71.4	22	4	AAW05144 Peptide #
21	5	71.4	22	5	ABG39271 Human pep
22	5	71.4	41	7	ADB81615 Human ova
23	5	71.4	45	8	ADS07258 Staphyloc

24	5	71.4	50	8	ADU79042	Adu79042 Human pro
25	5	71.4	62	5	ABP04426	Abp04426 Human ORF
26	5	71.4	64	4	ABG06841	Abg06841 Novel hum
27	5	71.4	67	5	ABP10817	Abp10817 Human ORF
28	5	71.4	70	7	ABO66622	AbO66622 Klebsiell
29	5	71.4	78	4	AAW95241	Aam95241 Human rep
30	5	71.4	78	4	ABB95938	Abb95938 Human tes
31	5	71.4	81	4	ABG06812	Abg06812 Novel hum
32	5	71.4	92	4	AAG71384	Aag71384 Human gen
33	5	71.4	99	4	ABG22770	Abg22770 Novel hum
34	5	71.4	101	4	AAU63061	Aau63061 Propionib
35	5	71.4	101	6	ABM59580	Abm59580 Propionib
36	5	71.4	111	4	ABG19849	Abg19849 Novel hum
37	5	71.4	120	5	ABP43071	Abp43071 Human ova
38	5	71.4	122	8	ADY05847	Ady05847 Plant ful
39	5	71.4	129	4	ABW94957	Abw94957 Human pro
40	5	71.4	129	6	ABU00255	Abu00255 Human nov
41	5	71.4	129	8	ADRI4686	Adri4686 Human NF-
42	5	71.4	131	8	ADM87692	Adm87692 Human EST
43	5	71.4	134	4	AAU31384	Aau31384 Novel hum
44	5	71.4	134	6	ABO00449	AbO00449 Novel hum
45	5	71.4	134	8	ADX88163	Adx88163 Plant ful
46	5	71.4	135	3	AAG16191	Aag16191 Arabidops
47	5	71.4	144	4	AAU30881	Aau30881 Novel hum
48	5	71.4	146	4	AAG65762	Aag65762 Putative
49	5	71.4	146	7	ADB64268	Adb64268 Human pro
50	5	71.4	146	7	ADP58647	Adp58647 Human pol
51	5	71.4	146	8	ABM81098	Abm81098 Tumour-as
52	5	71.4	146	8	ADY05516	Ady05516 Plant ful
53	5	71.4	150	8	ADR90527	Adr90527 Human ret
54	5	71.4	151	4	AAG91093	Aag91093 C glutami
55	5	71.4	151	9	AED71964	Aed71964 Corynebac
56	5	71.4	162	3	ABW51881	Abw51881 Human sec
57	5	71.4	162	8	ADX76620	Adx76620 Plant ful
58	5	71.4	163	7	ADD26756	Add26756 Human adi
59	5	71.4	164	3	AAW51880	Aaw51880 Gene 2 hu
60	5	71.4	166	3	AAG13319	Aag13319 Arabidops
61	5	71.4	172	4	ADY64822	Ady64822 S. manson
62	5	71.4	176	9	ADW64822	Adw64822 Murine Rb
63	5	71.4	177	3	AAG53487	Aag53487 Arabidops
64	5	71.4	177	3	AG08198	Ag08198 Arabidops
65	5	71.4	177	9	AED21447	Aed21447 Mouse-ear
66	5	71.4	177	9	AED61147	Aed61147 Thale cre
67	5	71.4	178	3	AAG27486	Aag27486 Arabidops
68	5	71.4	178	6	ABU43294	Abu43294 Protein e
69	5	71.4	191	3	AG13318	Ag13318 Arabidops
70	5	71.4	191	4	AAE13835	Aae13835 Human lun
71	5	71.4	191	5	ABP39865	Abp39865 Staphyloc
72	5	71.4	191	7	ADD66701	Add66701 Human lun
73	5	71.4	191	7	ADW59337	Adw59337 Human pro
74	5	71.4	191	7	ADD45625	Add45625 Human pro
75	5	71.4	191	7	ADW87955	Adw87955 Human lun
76	5	71.4	191	8	ADS06905	Ads06905 Staphyloc
77	5	71.4	191	8	ABM81895	Abm81895 Tumour-as
78	5	71.4	191	8	ADW88276	Adw88276 Human pro
79	5	71.4	194	4	AAU17534	Aau17534 Novel sig
80	5	71.4	194	4	AAU17111	Aau17111 Novel sig
81	5	71.4	194	7	ADB93819	Adb93819 Human nov
82	5	71.4	194	7	ADB94242	Adb94242 Human nov
83	5	71.4	200	8	ADR90533	Adr90533 Human ret
84	5	71.4	201	3	AAG53486	Aag53486 Arabidops
85	5	71.4	202	3	AG08197	Ag08197 Arabidops
86	5	71.4	202	7	ADD26797	Add26797 Human adi
87	5	71.4	204	8	ADM72128	Adm72128 Human NTR
88	5	71.4	207	8	ADR90538	Adr90538 Human ret
89	5	71.4	208	8	ADR90532	Adr90532 Human ret
90	5	71.4	211	3	ABG27485	Abg27485 Arabidops
91	5	71.4	219	4	ABW64552	Abw64552 Drosophil
92	5	71.4	224	2	AAW36516	Aaw36516 Human syn
93	5	71.4	224	2	AAW41709	Aaw41709 Human PRO
94	5	71.4	224	3	AAW40802	Aaw40802 Human ORF
95	5	71.4	224	3	AAW44265	Aaw44265 Human PRO
96	5	71.4	224	3	AAW24048	Aaw24048 Human PRO

97	5	71.4	224	4	AAB64539	Aab64539	Gene 45 h	170	5	71.4	224	9	AED63934	Aed63934	Different
98	5	71.4	224	4	AAB64466	Aab64466	Human sec	171	5	71.4	225	7	ADP59585	Adp59585	Human pol
99	5	71.4	224	4	AAB64540	Aab64540	Human sec	172	5	71.4	225	7	ABM96257	Abm96257	M. xanthu
100	5	71.4	224	5	ABP03470	Abp03470	Human ORF	173	5	71.4	229	3	AAV74692	Aay74692	Neisseria
101	5	71.4	224	6	ABO25211	Abu25211	Novel hum	174	5	71.4	229	3	AAV74694	Aay74694	Neisseria
102	5	71.4	224	6	ABU72217	Abu72217	Novel hum	175	5	71.4	229	3	ABP79613	Abp79613	N. gonorr
103	5	71.4	224	6	ABU84897	Abu84897	Human sec	176	5	71.4	229	6	ABU37138	Abu37138	Protein e
104	5	71.4	224	6	ABU61095	Abu61095	Human PRO	177	5	71.4	229	6	ABU38067	Abu38067	Protein e
105	5	71.4	224	6	ABU80364	Abu80364	Human sec	178	5	71.4	231	2	AAO4747	Aar04747	Amino aci
106	5	71.4	224	6	ADA24701	Ada24701	Novel hum	179	5	71.4	231	2	ABG22771	Abg22771	Novel hum
107	5	71.4	224	6	ABO19666	Abu19666	Novel hum	180	5	71.4	233	9	ABM95205	Abm95205	M. xanthu
108	5	71.4	224	6	ADA12362	Ada12362	Human sec	181	5	71.4	234	7	ADH89335	Adh89335	Z. maye 1
109	5	71.4	224	6	ABO19557	Abu19557	Novel hum	182	5	71.4	234	8	ADG44121	Adg44121	Z. maye 1
110	5	71.4	224	7	ADB73668	Abd73668	Human PRO	183	5	71.4	235	2	AAR04748	Aar04748	Amino aci
111	5	71.4	224	7	ADB76384	Abd76384	Human PRO	184	5	71.4	240	3	AAB43978	Aab43978	Human can
112	5	71.4	224	7	ADC43810	Adc43810	Human sec	185	5	71.4	241	3	AGG27706	Agg27706	Arabiidops
113	5	71.4	224	7	ADC61570	Adc61570	Human sec	186	5	71.4	241	3	AGG27484	Agg27484	Arabiidops
114	5	71.4	224	7	ADC63534	Adc63534	Human sec	187	5	71.4	242	8	ADS30131	Ads30131	Bacterial
115	5	71.4	224	7	ADC66634	Adc66634	Human sec	188	5	71.4	250	8	ADK72425	Adk72425	Plant ful
116	5	71.4	224	7	ADC68758	Adc68758	Human sec	189	5	71.4	254	2	AAV42165	Aay42165	Human che
117	5	71.4	224	7	ADC62818	Adc62818	Human sec	190	5	71.4	254	2	AAB10491	Aab10491	Human CXC
118	5	71.4	224	7	ADC67883	Adc67883	Human sec	191	5	71.4	254	3	AAB34733	Aab34733	Human sec
119	5	71.4	224	7	ADC41203	Adc41203	Human sec	192	5	71.4	254	4	AAB68423	Aab68423	Amino aci
120	5	71.4	224	7	ADC67258	Adc67258	Human sec	193	5	71.4	254	4	AAB84199	Aab84199	Amino aci
121	5	71.4	224	7	ADC62194	Adc62194	Human sec	194	5	71.4	254	5	AAO14637	Aao14637	Amino aci
122	5	71.4	224	7	ADC41827	Adc41827	Human sec	195	5	71.4	254	5	ABB84955	Abb84955	Human PRO
123	5	71.4	224	7	ADD45142	Ad45142	Human PRO	196	5	71.4	254	5	ABB95561	Abb95561	Human ang
124	5	71.4	224	7	ADE54986	Ade54986	Human PRO	197	5	71.4	254	7	ADD10567	Add10567	Human sec
125	5	71.4	224	7	ADE49196	Ade49196	Human sec	198	5	71.4	254	7	ADD11527	Add11527	Human sec
126	5	71.4	224	7	ADE35250	Ade35250	Human sec	199	5	71.4	254	7	ADD37320	Add37320	Human sec
127	5	71.4	224	7	ADE16364	Ade16364	Human sec	200	5	71.4	254	7	ADG87435	Adg87435	Human che
128	5	71.4	224	7	ADD72979	Ad72979	Human sec	201	5	71.4	254	7	ADG87437	Adg87437	Human sec
129	5	71.4	224	7	ADD72337	Ad72337	Human sec	202	5	71.4	254	7	ADZ51814	Adz51814	Human sca
130	5	71.4	224	7	ADD16988	Ad16988	Human sec	203	5	71.4	254	8	ADE41528	Ade41528	Human sec
131	5	71.4	224	7	ADF47002	Adf47002	Human sec	204	5	71.4	254	8	ADH43711	Adh43711	Human PRO
132	5	71.4	224	7	ADG52759	Adg52759	Human sec	205	5	71.4	258	8	ADA35702	Ada35702	Acinetoba
133	5	71.4	224	7	ADG60079	Adg60079	Human sec	206	5	71.4	261	4	AAB70543	Aab70543	Human PRO
134	5	71.4	224	7	ADI60839	Adi60839	Human sec	207	5	71.4	261	4	ABO01372	Abu01372	Human PRO
135	5	71.4	224	8	ADE48496	Ade48496	Human sec	208	5	71.4	261	6	ABO01373	Abu01373	Human PRO
136	5	71.4	224	8	ADE89597	Ade89597	Human sec	209	5	71.4	261	6	ABO01366	Abu01366	Human PRO
137	5	71.4	224	8	ADF61237	Adf61237	Human sec	210	5	71.4	261	8	ADN96118	Adn96118	Human NOV
138	5	71.4	224	8	ADF39929	Adf39929	Human sec	211	5	71.4	261	8	ADN96104	Adn96104	Human NOV
139	5	71.4	224	8	ADF45725	Adf45725	Human sec	212	5	71.4	261	8	ADN96116	Adn96116	Human NOV
140	5	71.4	224	8	ADF24121	Adf24121	Human sec	213	5	71.4	263	5	ABP39793	Abp39793	Staphyloc
141	5	71.4	224	8	ADF40553	Adf40553	Human sec	214	5	71.4	263	8	ADS05572	Ads05572	Staphyloc
142	5	71.4	224	8	ADF23497	Adf23497	Human sec	215	5	71.4	273	3	AAV57907	Aay57907	Human tra
143	5	71.4	224	8	ADF33480	Adf33480	Human sec	216	5	71.4	273	4	AAV57907	Aay57907	Human tra
144	5	71.4	224	8	ADF26947	Adf26947	Human sec	217	5	71.4	273	4	AAV57907	Aay57907	Human tra
145	5	71.4	224	8	ADF27583	Adf27583	Human sec	218	5	71.4	273	4	AAV57907	Aay57907	Human tra
146	5	71.4	224	8	ADF41177	Adf41177	Human sec	219	5	71.4	273	6	ABU08260	Abu08260	Human sto
147	5	71.4	224	8	ADF32856	Adf32856	Human sec	220	5	71.4	273	6	ADJ75419	Adj75419	Marker ge
148	5	71.4	224	8	ADF25222	Adf25222	Human sec	221	5	71.4	273	8	ADQ39835	Adq39835	Human myo
149	5	71.4	224	8	ADF26323	Adf26323	Human sec	222	5	71.4	275	8	ADQ59517	Adq59517	Human can
150	5	71.4	224	8	ADF34112	Adf34112	Human sec	223	5	71.4	279	4	AAV72625	Aay72625	Human ang
151	5	71.4	224	8	ADF46349	Adf46349	Human sec	224	5	71.4	290	7	ABO69586	Abu69586	Pseudomon
152	5	71.4	224	8	ADG50335	Adg50335	Human sec	225	5	71.4	291	6	ABP71288	Abp71288	Common re
153	5	71.4	224	8	ADG49711	Adg49711	Human sec	226	5	71.4	297	6	ABP70972	Abp70972	Epoxide h
154	5	71.4	224	8	ADG51583	Adg51583	Human sec	227	5	71.4	297	6	ABD07626	Abd07626	Alloicoc
155	5	71.4	224	8	ADG49087	Adg49087	Human sec	228	5	71.4	297	6	ADU00280	Adu00280	Epoxide h
156	5	71.4	224	8	ADG48463	Adg48463	Human sec	229	5	71.4	300	6	ADA26915	Ada26915	Mouse the
157	5	71.4	224	8	ADG50959	Adg50959	Human sec	230	5	71.4	300	6	ADA26915	Ada26915	Mouse the
158	5	71.4	224	8	ADG58903	Adg58903	Human sec	231	5	71.4	302	3	AAV97213	Aay97213	Mouse PGC
159	5	71.4	224	8	ADG62359	Adg62359	Human sec	232	5	71.4	302	3	AAV97213	Aay97213	Campyloba
160	5	71.4	224	8	ADH25384	Adh25384	Human neu	233	5	71.4	302	6	ABJ18492	Abj18492	Campyloba
161	5	71.4	224	8	ADM17161	Adm17161	Human sec	234	5	71.4	302	6	ABD07628	Abd07628	Alloicoc
162	5	71.4	224	8	ADL06995	Adl06995	Human sec	235	5	71.4	303	6	ABU26594	Abu26594	Protein e
163	5	71.4	224	8	ADL91853	Adl91853	Human PRO	236	5	71.4	304	3	AAV26472	Aay26472	Arabiidops
164	5	71.4	224	8	ADP54173	Adp54173	Human PRO	237	5	71.4	306	4	ABB69724	Abb69724	Drosophila
165	5	71.4	224	8	ADT91094	Adt91094	Human PRO	238	5	71.4	310	6	ABU15108	Abu15108	Protein e
166	5	71.4	224	8	ADU50117	Adu50117	PRO615, S	239	5	71.4	312	4	AAV22968	Aay22968	Human olf
167	5	71.4	224	9	ADW49396	Adw49396	PRO615 pr	240	5	71.4	314	6	ABP75962	Abp75962	Human sec
168	5	71.4	224	9	ADZ52057	Adz52057	Human sec	241	5	71.4	317	6	ADA35598	Ada35598	Acinetoba
169	5	71.4	224	9	AED47885	Aed47885	Human PRO	242	5	71.4	320	6	ABP71289	Abp71289	Mouse the

GenCore version 5.1.9
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 OM protein - protein search, using sw model
 Run on: October 13, 2006, 01:20:08 ; Search time 186 Seconds
 (without alignments)
 17.433 Million cell updates/sec

Title: US-10-537-648-1

Perfect score: 7

Sequence: 1 YLTQPS 7

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 2097797 seqs, 463214858 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2072432

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Published Applications AA.Main.*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	85.7	87	4	US-10-425-115-291176 Sequence 291176,
2	6	85.7	119	4	US-10-425-115-224207 Sequence 224207,
3	6	85.7	415	5	US-10-501-282-2354 Sequence 2354, Ap
4	6	85.7	503	5	US-10-501-282-2356 Sequence 2356, Ap
5	6	85.7	717	5	US-10-501-282-2358 Sequence 2358, Ap
6	6	85.7	1375	3	US-09-808-602-66 Sequence 66, Appl
7	6	85.7	1375	3	US-09-800-198-55 Sequence 55, Appl
8	6	85.7	1526	6	US-11-097-143-18609 Sequence 18609, A
9	5	71.4	10	3	US-09-827-345-8 Sequence 8, Appl
10	5	71.4	10	4	US-10-227-616-47 Sequence 47, Appl
11	5	71.4	10	6	US-11-220-407-8 Sequence 8, Appl
12	5	71.4	22	3	US-09-864-761-37126 Sequence 37126, A
13	5	71.4	41	5	US-10-487-561-104 Sequence 104, App
14	5	71.4	42	4	US-10-425-115-253500 Sequence 253500,
15	5	71.4	45	4	US-10-724-972A-6553 Sequence 6553, Ap
16	5	71.4	45	4	US-10-425-115-283377 Sequence 283377,
17	5	71.4	50	4	US-10-425-115-21966 Sequence 21966,
18	5	71.4	50	5	US-10-776-013-415 Sequence 415, App
19	5	71.4	51	4	US-10-424-599-206558 Sequence 206558,
20	5	71.4	53	4	US-10-425-115-215732 Sequence 215732,
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22	5	71.4	55	4	US-10-425-115-311628 Sequence 311628,
23	5	71.4	56	4	US-10-437-963-204269 Sequence 204269,
24	5	71.4	64	5	US-10-450-763-37200 Sequence 37200, A
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 Sequence 191446,
 Sequence 10, Appl
 Sequence 2422, Ap
 Sequence 61331, A
 Sequence 2424, Ap
 Sequence 4847, Ap
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OM protein - protein search, using sw model

Run on: October 13, 2006, 01:06:47 ; Search time 38 Seconds
(without alignments)
14.627 Million cell updates/sec

Title: US-10-537-648-1

Perfect score: 37

Sequence: 1 YLTQPOS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 295242 seqs, 79405279 residues

Total number of hits satisfying chosen parameters: 295242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA New.*

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- 2: /EMC_Celerra_SID33/ptodata/2/pubpaa/US06_NEW_PUB pep.*
- 3: /EMC_Celerra_SID33/ptodata/2/pubpaa/US07_NEW_PUB pep.*
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- 8: /EMC_Celerra_SID33/ptodata/2/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	32	86.5	264	7	US-11-056-3558-105138
4	32	86.5	264	7	US-11-056-3558-116377
5	32	86.5	312	7	US-11-056-3558-37814
6	32	86.5	312	7	US-11-056-3558-105137
7	32	86.5	312	7	US-11-056-3558-116376
8	32	86.5	928	7	US-11-315-777-8
9	32	86.5	928	7	US-11-319-873-8
10	32	86.5	928	7	US-11-324-926-8
11	30	81.1	98	6	US-10-449-902-50568
12	30	81.1	303	6	US-10-449-902-30928
13	30	81.1	563	6	US-10-449-902-43710
14	30	81.1	563	6	US-10-449-902-53474
15	30	81.1	1013	6	US-10-449-902-45687
16	29	78.4	218	7	US-11-056-3558-91402
17	29	78.4	218	7	US-11-056-3558-95158
18	29	78.4	222	7	US-11-056-3558-91401
19	29	78.4	222	7	US-11-056-3558-95157
20	29	78.4	228	7	US-11-056-3558-91400
21	29	78.4	228	7	US-11-056-3558-95156
22	29	78.4	293	6	US-10-526-572-17
23	29	78.4	324	7	US-11-330-403-7912
24	29	78.4	403	6	US-10-953-349-3753
25	29	78.4	406	6	US-10-953-349-3752

26	29	78.4	422	6	US-10-953-349-3751	Sequence 3751, Ap
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38	28	75.7	758	6	US-10-474-894-12	Sequence 17, Appl
39	28	75.7	765	7	US-11-056-3558-82533	Sequence 82533, A
40	28	75.7	777	7	US-11-056-3558-86579	Sequence 86579, A
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75	27	73.0	395	7	US-11-056-3558-115163	Sequence 115163, A
76	27	73.0	397	7	US-11-330-403-3473	Sequence 3473, Ap
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90	27	73.0	444	7	US-11-056-3558-103922	Sequence 103922, A
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92	27	73.0	490	7	US-11-056-3558-3587	Sequence 3587, Ap
93	27	73.0	531	6	US-10-449-902-50801	Sequence 50801, A
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106	27	73.0	1352	6	US-10-511-302A-42	Sequence 42, Appl	179	26	70.3	836	6	US-11-313-104-16	Sequence 16, Appl
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114	26	70.3	173	7	US-11-192-046-93	Sequence 93, Appl	187	26	70.3	918	6	US-10-449-902-47854	Sequence 47854, A
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132	26	70.3	307	7	US-11-434-184-2758	Sequence 2758, Ap	205	26	70.3	1414	7	US-11-051-725-2	Sequence 2, Appl
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138	26	70.3	326	6	US-11-056-355B-53527	Sequence 53527, A	211	26	70.3	2353	6	US-10-543-503-130	Sequence 130, App
139	26	70.3	369	6	US-10-449-902-36632	Sequence 36632, A	212	26	70.3	2353	6	US-11-051-725-119	Sequence 119, App
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OM protein - protein search, using sw model

Run on: October 13, 2006, 00:54:56 ; Search time 199 Seconds
(without alignments)
16.083 Million cell updates/sec

Title: US-10-537-648-1

Perfect score: 37

Sequence: 1 YLTQPOS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database:

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8: Geneseq2004s.*

9: Geneseq2005s.*

10: Geneseq2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	37	100.0	7	8	Adg16409 Amino aci
2	33	89.2	331	8	Adn18451 Bacterial
3	33	89.2	371	7	Adf04626 Bacterial
4	33	89.2	415	6	Adb08414 Alloiococ
5	33	89.2	503	6	Adb08416 Alloiococ
6	33	89.2	717	6	Adb08418 Alloiococ
7	32	86.5	250	8	Adr90527 Human ret
8	32	86.5	172	4	Adb66919 Murine Rb
9	32	86.5	200	8	Adr90533 Human ret
10	32	86.5	207	8	Adr90538 Human ret
11	32	86.5	208	8	Adr90532 Human ret
12	32	86.5	264	3	Aag42941 Arabidops
13	32	86.5	264	3	Aag05410 Arabidops
14	32	86.5	264	8	Adt56245 Plant pol
15	32	86.5	312	3	Aag42940 Arabidops
16	32	86.5	312	3	Aag05409 Arabidops
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18	32	86.5	781	6	Abus58789 Human ret
19	32	86.5	816	1	Aap82112 Human ret
20	32	86.5	816	2	Aar63584 Retinobla
21	32	86.5	816	2	Aar58568 Human ret
22	32	86.5	816	2	Aaw71355 Protein s
23	32	86.5	816	2	Aay01542 Human ret

24	32	86.5	816	6	ABUS8784	Abus8784 Human ret
25	32	86.5	832	2	AAW69368	AAW69368 Modified
26	32	86.5	832	6	ABUS8788	Abus8788 Human ret
27	32	86.5	851	2	AAW69370	AAW69370 Modified
28	32	86.5	851	2	AAW69367	AAW69367 Modified
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30	32	86.5	851	6	ABUS8787	Abus8787 Human ret
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32	32	86.5	869	6	ABUS8794	Abus8794 Human ret
33	32	86.5	871	2	AAW69375	AAW69375 Modified
34	32	86.5	871	6	ABUS8795	Abus8795 Human ret
35	32	86.5	874	6	AAW69366	AAW69366 Modified
36	32	86.5	874	6	ABUS8786	Abus8786 Human ret
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43	32	86.5	899	7	ADE56023	Ades6023 Rat Prote
44	32	86.5	899	7	ADE56007	Ades6007 Rat Prote
45	32	86.5	899	7	ADE56011	Ades6011 Rat Prote
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54	32	86.5	928	2	AAW71681	Aar71681 Recombina
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92	32	86.5	928	9	ADW20876	Adw20876 Retinobla
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94	32	86.5	928	9	ADY19477	Ady19477 PRO polypp
95	32	86.5	928	9	ABE55610	Aeb55610 Human ret
96	32	86.5	928	9	ABE21880	Aec21880 Human ret

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98	32	86.5	970	1	AAP90599	Aap90599 Human ret	171	29	78.4	224	6	ABO19666	Abol19666 Novel hum
99	31	83.8	66	6	AUA9143	Aua9143 Propionib	172	29	78.4	224	6	ADA12362	Ada12362 Human sec
100	31	83.8	66	6	ABM45662	Abm45662 Propionib	173	29	78.4	224	6	ABO19557	Abol19557 Novel hum
101	31	83.8	128	4	ABG02275	Abg02275 Novel hum	174	29	78.4	224	7	ABD73668	Abd73668 Human PRO
102	31	83.8	224	3	AAB40802	Aab40802 Human ORF	175	29	78.4	224	7	ADB76384	Adb76384 Human PRO
103	31	83.8	224	5	ABP03470	Abp03470 Human ORF	176	29	78.4	224	7	ADC43810	Adc43810 Human sec
104	31	83.8	339	6	ABU17118	Abu17118 Protein e	177	29	78.4	224	7	ADG61570	Adg61570 Human sec
105	31	83.8	361	6	ADA36646	Ada36646 Acinetoba	178	29	78.4	224	7	ADC63534	Adc63534 Human sec
106	31	83.8	508	8	ADQ67799	Adq67799 Novel hum	179	29	78.4	224	7	ADC66634	Adc66634 Human sec
107	31	83.8	549	8	ABO79802	Abol79802 Pseudomon	180	29	78.4	224	7	ADC68758	Adc68758 Human sec
108	31	83.8	562	5	ABP73802	Abp73802 Candida a	181	29	78.4	224	7	ADC62818	Adc62818 Human sec
109	31	83.8	714	4	AAG70834	Aag70834 C albican	182	29	78.4	224	7	ADC67883	Adc67883 Human sec
110	31	83.8	776	4	AUA1553	Aua1553 Propionib	183	29	78.4	224	7	ADC41203	Adc41203 Human sec
111	31	83.8	776	4	ABM38072	Abm38072 Propionib	184	29	78.4	224	7	ADC67258	Adc67258 Human sec
112	31	83.8	1047	4	ABB67483	Abb67483 Drosophil	185	29	78.4	224	7	ADC62194	Adc62194 Human sec
113	30	81.1	162	8	ADX76620	Adx76620 Plant ful	186	29	78.4	224	7	ADC41827	Adc41827 Human sec
114	30	81.1	204	6	ADA36645	Ada36645 Acinetoba	187	29	78.4	224	7	ADD45142	Add45142 Human PRO
115	30	81.1	341	6	ADB06882	Adb06882 Alloiococ	188	29	78.4	224	7	ADE54986	Ade54986 Human PRO
116	30	81.1	345	6	ADB06884	Adb06884 Alloiococ	189	29	78.4	224	7	ADE49196	Ade49196 Human sec
117	30	81.1	421	7	ABO63138	Abol63138 Klebsiell	190	29	78.4	224	7	ADG35250	Adg35250 Human sec
118	30	81.1	437	8	ADX73491	Adx73491 Plant ful	191	29	78.4	224	7	ADG16364	Adg16364 Human sec
119	30	81.1	528	4	AAG81143	Aag81143 Mycobacte	192	29	78.4	224	7	ADD72979	Add72979 Human sec
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121	30	81.1	528	6	ABU34906	Abu34906 Protein e	194	29	78.4	224	7	ADG16988	Adg16988 Human sec
122	30	81.1	538	7	ADC61131	Adc61131 Baeys-Vi	195	29	78.4	224	7	ADP47002	Adp47002 Human sec
123	30	81.1	553	9	ABP39586	Abp39586 L. pneumo	196	29	78.4	224	7	ADG52759	Adg52759 Human sec
124	30	81.1	574	9	ABP36163	Abp36163 L. pneumo	197	29	78.4	224	7	ADG60079	Adg60079 Human sec
125	30	81.1	639	4	AUA71928	Aua71928 Human bon	198	29	78.4	224	7	ADG160839	Adg160839 Human sec
126	30	81.1	705	6	ABU49632	Abu49632 Protein e	199	29	78.4	224	8	ADE48496	Ade48496 Human sec
127	30	81.1	738	8	ADP99038	Adp99038 C. albica	200	29	78.4	224	8	ADP61237	Adp61237 Human sec
128	30	81.1	1200	3	AAG30768	Aag30768 Arabidops	201	29	78.4	224	8	ADP39929	Adp39929 Human sec
129	30	81.1	1207	3	AAG30766	Aag30766 Arabidops	202	29	78.4	224	8	ADP45725	Adp45725 Human sec
130	30	81.1	1215	3	ABG30766	Abg30766 Arabidops	203	29	78.4	224	8	ADP45725	Adp45725 Human sec
131	30	81.1	1526	4	ABG39339	Abg39339 Drosophil	204	29	78.4	224	8	ADP24121	Adp24121 Human sec
132	29	78.4	10	2	AAU25909	Aau25909 Beta-2-mi	205	29	78.4	224	8	ADF40553	Adf40553 Human sec
133	29	78.4	10	4	AAU25775	Aau25775 Breast Ca	206	29	78.4	224	8	ADF23497	Adf23497 Human sec
134	29	78.4	39	6	ABR47819	Abra47819 Human sec	207	29	78.4	224	8	ADP26947	Adp26947 Human sec
135	29	78.4	39	6	ABR00113	Abra00113 Human gen	208	29	78.4	224	8	ADP27583	Adp27583 Human sec
136	29	78.4	39	7	ABD91590	Abd91590 Human sec	209	29	78.4	224	8	ADP27583	Adp27583 Human sec
137	29	78.4	39	7	ADP27583	Adp27583 Human sec	210	29	78.4	224	8	ADP27583	Adp27583 Human sec
138	29	78.4	40	2	AAU07931	Aau07931 Human sec	211	29	78.4	224	8	ADP26323	Adp26323 Human sec
139	29	78.4	47	5	ABP69637	Abp69637 Human pol	212	29	78.4	224	8	ADP26323	Adp26323 Human sec
140	29	78.4	49	5	ABP43150	Abp43150 Human ova	213	29	78.4	224	8	ADP34112	Adp34112 Human sec
141	29	78.4	57	4	AAU00774	Aau00774 Human bon	214	29	78.4	224	8	ADP46349	Adp46349 Human sec
142	29	78.4	77	4	AAU99843	Aau99843 Human exc	215	29	78.4	224	8	ADG50335	Adg50335 Human sec
143	29	78.4	77	4	AAU42658	Aau42658 Human kid	216	29	78.4	224	8	ADG49711	Adg49711 Human sec
144	29	78.4	81	4	ABG06812	Abg06812 Novel hum	217	29	78.4	224	8	ADG51583	Adg51583 Human sec
145	29	78.4	81	4	ABG22770	Abg22770 Novel hum	218	29	78.4	224	8	ADG49087	Adg49087 Human sec
146	29	78.4	111	4	ABG19849	Abg19849 Novel hum	219	29	78.4	224	8	ADG48463	Adg48463 Human sec
147	29	78.4	134	8	ADX88163	Adx88163 Plant ful	220	29	78.4	224	8	ADG50959	Adg50959 Human sec
148	29	78.4	146	8	ADY05516	Ady05516 Plant ful	221	29	78.4	224	8	ADG58903	Adg58903 Human sec
149	29	78.4	153	8	ADG61779	Adg61779 Transcrip	222	29	78.4	224	8	ADG62359	Adg62359 Human sec
150	29	78.4	160	4	AAU18472	Aau18472 Human end	223	29	78.4	224	8	ADH25384	Adh25384 Human neu
151	29	78.4	162	3	ABP51881	Abp51881 Human sec	224	29	78.4	224	8	ADM17161	Adm17161 Human sec
152	29	78.4	184	3	ABP51880	Abp51880 Gene 2 hu	225	29	78.4	224	8	ADL06995	Adl06995 Human sec
153	29	78.4	178	6	AAU43294	Aau43294 Protein e	226	29	78.4	224	8	ADL1853	Adl1853 Human PRO
154	29	78.4	187	8	ABP39865	Abp39865 Lung spec	227	29	78.4	224	8	ADP54173	Adp54173 Human PRO
155	29	78.4	191	5	ABP39865	Abp39865 Staphyloc	228	29	78.4	224	8	ADU91094	Adu91094 Human PRO
156	29	78.4	191	8	ADG06905	Adg06905 Staphyloc	229	29	78.4	224	8	ADU50117	Adu50117 PRO615, S
157	29	78.4	204	8	ADM72128	Adm72128 Human NTR	230	29	78.4	224	9	ADM49396	Adm49396 PRO615 pr
158	29	78.4	224	2	AAU36516	Aau36516 Human syn	231	29	78.4	224	9	ADM49396	Adm49396 PRO615 pr
159	29	78.4	224	2	AAU41709	Aau41709 Human PRO	232	29	78.4	224	9	ADM49396	Adm49396 PRO615 pr
160	29	78.4	224	2	AAU44265	Aau44265 Human PRO	233	29	78.4	224	9	ADM49396	Adm49396 PRO615 pr
161	29	78.4	224	3	AAU44048	Aau44048 Human PRO	234	29	78.4	224	9	ADM49396	Adm49396 PRO615 pr
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165	29	78.4	224	6	ABO25211	Abol25211 Novel hum	238	29	78.4	224	9	ADM49396	Adm49396 PRO615 pr
166	29	78.4	224	6	ABU72217	Abu72217 Novel hum	239	29	78.4	224	9	ADM49396	Adm49396 PRO615 pr
167	29	78.4	224	6	ABU84897	Abu84897 Human sec	240	29	78.4	224	9	ADM49396	Adm49396 PRO615 pr
168	29	78.4	224	6	ABU61095	Abu61095 Human PRO	241	29	78.4	224	9	ADM49396	Adm49396 PRO615 pr
169	29	78.4	224	6	ABU80364	Abu80364 Human sec	242	29	78.4	224	9	ADM49396	Adm49396 PRO615 pr

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OM protein - protein search, using sw model

Run on: October 13, 2006, 01:05:12 ; Search time 52 Seconds
(without alignments)
11.783 Million cell updates/sec

Title: US-10-537-648-1

Perfect score: 37

Sequence: 1 YLTQPOS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued Patents_AA:*

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- 2: /EMC_Celerra_SIDS3/ptodata/2/aaa/6 COMB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/aaa/7 COMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/aaa/H COMB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/aaa/PCTUS_COMB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/aaa/RE_COMB.pep.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/aaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	33	89.2	371	US-09-543-681A-4911	Sequence 4911, Ap
2	32	86.5	816	US-08-038-760-3	Sequence 3, Appli
3	32	86.5	816	US-08-470-091-3	Sequence 3, Appli
4	32	86.5	928	US-08-504-329-1	Sequence 1, Appli
5	32	86.5	928	US-08-959-638-8	Sequence 8, Appli
6	32	86.5	928	US-08-482-627-5	Sequence 5, Appli
7	32	86.5	928	US-08-801-092-4	Sequence 4, Appli
8	32	86.5	928	US-08-328-673A-8	Sequence 8, Appli
9	32	86.5	928	US-09-315-113-4	Sequence 4, Appli
10	32	86.5	928	US-08-354-221-8	Sequence 8, Appli
11	32	86.5	928	US-09-315-116-4	Sequence 4, Appli
12	32	86.5	928	US-09-758-007-3	Sequence 3, Appli
13	32	86.5	928	US-10-441-510-8	Sequence 8, Appli
14	32	86.5	928	PCT-US94-10357-2	Sequence 2, Appli
15	32	86.5	928	PCT-US94-10357-3	Sequence 3, Appli
16	31	83.8	248	US-09-248-796A-1541	Sequence 1541, A
17	31	83.8	324	US-09-248-796A-15950	Sequence 15950, A
18	31	83.8	361	US-09-328-352-7933	Sequence 7933, Ap
19	31	83.8	549	US-09-252-991A-28548	Sequence 28548, A
20	30	81.1	204	US-09-328-352-7932	Sequence 7932, Ap
21	30	81.1	421	US-09-489-039A-9655	Sequence 9655, Ap
22	30	81.1	455	US-08-248-796A-16498	Sequence 16498, A
23	30	81.1	528	US-09-712-363-194	Sequence 194, App
24	30	81.1	681	US-09-270-767-42824	Sequence 42824, A
25	30	81.1	721	US-09-248-796A-16497	Sequence 16497, A
26	29	78.4	191	US-09-134-001C-4710	Sequence 4710, Ap

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28	78.4	224	2	US-09-999-833A-162	Sequence 162, App
29	78.4	224	2	US-10-020-445A-162	Sequence 162, App
30	78.4	224	2	US-09-978-189-162	Sequence 162, App
31	78.4	224	2	US-10-017-085A-162	Sequence 162, App
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35	78.4	356	2	US-09-949-016-10959	Sequence 10959, A
36	78.4	356	2	US-09-949-016-10960	Sequence 10960, A
37	78.4	357	1	US-08-612-986-5	Sequence 5, Appli
38	78.4	357	1	US-08-361-806A-5	Sequence 5, Appli
39	78.4	357	1	PCT-US95-16806A-5	Sequence 5, Appli
40	78.4	70	2	US-09-489-039A-13139	Sequence 13139, A
41	78.4	73	2	US-09-655-270A-32	Sequence 32, Appli
42	78.4	151	2	US-09-605-703B-2140	Sequence 2140, Ap
43	78.4	163	2	US-09-248-796A-16520	Sequence 16520, A
44	78.4	191	2	US-09-854-133-393	Sequence 393, App
45	78.4	195	2	US-09-213-293D-19	Sequence 19, Appli
46	78.4	204	2	US-09-270-767-59105	Sequence 59105, A
47	78.4	254	2	US-09-449-437A-4	Sequence 4, Appli
48	78.4	254	2	US-09-449-437A-6	Sequence 6, Appli
49	78.4	254	2	US-09-195-106-2	Sequence 2, Appli
50	78.4	263	2	US-09-134-001C-4638	Sequence 4638, Ap
51	78.4	290	2	US-09-252-991A-18332	Sequence 18332, A
52	78.4	303	2	US-09-495-406-17	Sequence 17, Appli
53	78.4	303	2	US-09-816-028A-29	Sequence 29, Appli
54	78.4	303	2	US-10-303-162-29	Sequence 29, Appli
55	78.4	303	2	US-10-303-134-29	Sequence 29, Appli
56	78.4	303	2	US-10-303-118-29	Sequence 29, Appli
57	78.4	303	3	US-10-735-419-29	Sequence 29, Appli
58	78.4	317	2	US-09-328-352-6885	Sequence 6885, Ap
59	78.4	330	2	US-09-710-279-1086	Sequence 1086, Ap
60	78.4	330	2	US-09-134-001C-3294	Sequence 3294, Ap
61	78.4	352	2	US-09-328-352-4559	Sequence 4559, Ap
62	78.4	363	2	US-10-104-047-3425	Sequence 3425, Ap
63	78.4	408	2	US-09-949-016-9941	Sequence 9941, Ap
64	78.4	435	2	US-09-856-061-2	Sequence 2, Appli
65	78.4	451	2	US-09-902-540-13988	Sequence 13988, A
66	78.4	453	2	US-09-270-767-43715	Sequence 43715, A
67	78.4	529	2	US-09-489-039A-8092	Sequence 8092, Ap
68	78.4	584	2	US-09-328-352-7872	Sequence 7872, Ap
69	78.4	702	2	US-09-232-200-102	Sequence 102, App
70	78.4	702	2	US-09-232-197-102	Sequence 102, App
71	78.4	702	2	US-09-232-201-102	Sequence 102, App
72	78.4	702	2	US-09-232-195-102	Sequence 102, App
73	78.4	702	3	US-09-405-504A-102	Sequence 102, App
74	78.4	710	2	US-09-107-532A-5067	Sequence 5067, Ap
75	78.4	730	2	US-09-999-833A-102	Sequence 102, App
76	78.4	730	2	US-10-020-445A-102	Sequence 102, App
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81	78.4	730	3	US-10-013-917A-102	Sequence 102, App
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83	78.4	990	2	US-10-094-749-2568	Sequence 2568, Ap
84	78.4	1082	1	US-08-106-493A-2	Sequence 2, Appli
85	78.4	1082	1	US-08-429-264-2	Sequence 2, Appli
86	78.4	1139	1	US-08-832-883-2	Sequence 2, Appli
87	78.4	1139	1	US-08-832-877-2	Sequence 2, Appli
88	78.4	1196	2	US-09-275-252A-9	Sequence 9, Appli
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90	78.4	1236	2	US-09-519-076-21	Sequence 21, Appli
91	78.4	1262	2	US-09-176-664-22	Sequence 22, Appli
92	78.4	1262	2	US-09-519-076-22	Sequence 22, Appli
93	78.4	1262	2	US-09-248-796A-24467	Sequence 24467, A
94	78.4	94	2	US-09-149-476-505	Sequence 505, App
95	78.4	99	2	US-08-956-171E-5223	Sequence 5223, Ap
96	78.4	99	2	US-08-781-986A-5223	Sequence 5223, Ap
97	78.4	157	2	US-09-328-352-5951	Sequence 5951, Ap
98	78.4	160	2	US-09-270-767-49066	Sequence 49066, A
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100	27	73.0	161	2	US-09-270-767-33849	Sequence 33849, A	173	26	70.3	297	2	US-10-272-490-32	Sequence 32, Appl
101	27	73.0	168	2	US-09-602-777A-88	Sequence 88, Appl	174	26	70.3	297	2	US-10-214-473-32	Sequence 32, Appl
102	27	73.0	173	2	US-09-248-796A-17745	Sequence 17745, A	175	26	70.3	306	2	US-09-584-568C-11	Sequence 11, Appl
103	27	73.0	180	2	US-09-270-767-44236	Sequence 44236, A	176	26	70.3	308	2	US-09-328-352-7061	Sequence 7061, Ap
104	27	73.0	220	2	US-09-252-991A-24796	Sequence 24796, A	177	26	70.3	335	2	US-09-489-039A-9285	Sequence 9285, Ap
105	27	73.0	233	2	US-09-902-540-14404	Sequence 14404, A	178	26	70.3	348	2	US-09-216-295-16	Sequence 16, Appl
106	27	73.0	243	2	US-09-270-767-33470	Sequence 33470, A	179	26	70.3	348	2	US-09-632-570-16	Sequence 16, Appl
107	27	73.0	243	2	US-09-270-767-48687	Sequence 48687, A	180	26	70.3	348	2	US-09-632-575-46	Sequence 46, Appl
108	27	73.0	283	2	US-09-252-991A-20071	Sequence 20071, A	181	26	70.3	355	2	US-09-540-236-3814	Sequence 3814, Ap
109	27	73.0	348	2	US-09-495-880A-13	Sequence 13, Appl	182	26	70.3	358	2	US-09-543-681A-4765	Sequence 4765, Ap
110	27	73.0	348	2	US-09-495-880A-28	Sequence 28, Appl	183	26	70.3	385	2	US-09-524-101D-2	Sequence 2, Appli
111	27	73.0	348	2	US-09-495-880A-33	Sequence 33, Appl	184	26	70.3	386	2	US-09-724-623-92	Sequence 92, Appl
112	27	73.0	358	2	US-09-107-532A-4143	Sequence 4143, Ap	185	26	70.3	386	2	US-09-270-767-42532	Sequence 42532, A
113	27	73.0	358	2	US-09-248-796A-22578	Sequence 22578, A	186	26	70.3	386	3	US-10-288-930-92	Sequence 92, Appl
114	27	73.0	421	2	US-09-198-452A-535	Sequence 535, App	187	26	70.3	387	2	US-09-252-991A-22990	Sequence 22990, A
115	27	73.0	422	2	US-09-248-796A-16512	Sequence 16512, A	188	26	70.3	396	2	US-09-248-796A-20944	Sequence 20944, A
116	27	73.0	429	2	US-09-438-185A-497	Sequence 497, App	189	26	70.3	402	2	US-09-489-039A-13886	Sequence 13886, A
117	27	73.0	433	2	US-09-248-796A-24548	Sequence 24548, A	190	26	70.3	405	2	US-09-719-088B-3	Sequence 3, Appli
118	27	73.0	437	2	US-09-602-777A-84	Sequence 84, Appl	191	26	70.3	408	2	US-09-719-088B-3	Sequence 2, Appli
119	27	73.0	449	2	US-09-248-796A-18862	Sequence 18862, A	192	26	70.3	420	2	US-09-255-368-6	Sequence 6, Appli
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123	27	73.0	536	2	US-09-107-433-2945	Sequence 2945, Ap	196	26	70.3	441	2	US-09-248-796A-18617	Sequence 18617, A
124	27	73.0	602	2	US-09-248-796A-20214	Sequence 20214, A	197	26	70.3	443	2	US-09-328-352-7567	Sequence 7567, Ap
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126	27	73.0	754	2	US-09-270-767-44479	Sequence 44479, A	199	26	70.3	446	2	US-09-270-767-48415	Sequence 48415, A
127	27	73.0	761	3	US-10-114-270-108	Sequence 108, App	200	26	70.3	448	2	US-09-270-767-58387	Sequence 58387, A
128	27	73.0	787	2	US-09-489-039A-7628	Sequence 7628, Ap	201	26	70.3	448	2	US-09-710-279-996	Sequence 996, App
129	27	73.0	881	2	US-09-489-039A-12003	Sequence 12003, A	202	26	70.3	454	2	US-09-605-703B-82	Sequence 82, Appl
130	27	73.0	937	2	US-09-543-681A-5513	Sequence 5513, Ap	203	26	70.3	454	2	US-09-605-703B-84	Sequence 84, Appl
131	27	73.0	2441	1	US-08-194-468-2	Sequence 2, Appli	204	26	70.3	455	2	US-09-134-001C-3653	Sequence 3653, Ap
132	27	73.0	2441	2	US-08-961-739-2	Sequence 2, Appli	205	26	70.3	455	2	US-09-240-639-2	Sequence 2, Appli
133	27	73.0	2441	2	US-09-514-247A-8	Sequence 8, Appli	206	26	70.3	456	2	US-09-908-510A-2	Sequence 2, Appli
134	27	73.0	2441	2	US-09-686-316-2	Sequence 2, Appli	207	26	70.3	456	2	US-09-905-744B-2	Sequence 2, Appli
135	27	73.0	2442	2	US-09-514-247A-10	Sequence 10, Appl	208	26	70.3	456	2	US-10-107-860-2	Sequence 2, Appli
136	27	73.0	2442	2	US-09-538-092-1370	Sequence 1370, Ap	209	26	70.3	456	2	US-10-107-860-2	Sequence 2, Appli
137	27	73.0	3672	1	US-08-822-445-12	Sequence 12, Appl	210	26	70.3	456	2	US-09-905-732B-2	Sequence 2, Appli
138	27	73.0	3672	2	US-09-396-540-12	Sequence 12, Appl	211	26	70.3	456	2	US-09-905-732B-2	Sequence 2, Appli
139	27	73.0	3801	1	US-08-822-445-10	Sequence 10, Appl	212	26	70.3	456	2	US-09-905-589-2	Sequence 2, Appli
140	27	73.0	3801	2	US-09-396-540-10	Sequence 10, Appl	213	26	70.3	456	2	US-10-108-171A-2	Sequence 2, Appli
141	26	70.3	62	2	US-09-302-626B-32	Sequence 32, Appl	214	26	70.3	484	2	US-09-608-285A-27	Sequence 27, Appl
142	26	70.3	86	2	US-09-621-976-6132	Sequence 6132, Ap	215	26	70.3	484	2	US-09-370-265-27	Sequence 27, Appl
143	26	70.3	86	2	US-09-302-626B-34	Sequence 34, Appl	216	26	70.3	484	2	US-09-557-800C-27	Sequence 27, Appl
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160	4	57.1	21	2	US-09-563-222C-98	Sequence 98, Appl	233	4	57.1	69	7	5217896-5	Patent No. 5217896
161	4	57.1	21	2	US-09-563-222C-101	Sequence 101, App	234	4	57.1	70	2	US-09-205-258-1160	Sequence 1160, Ap
162	4	57.1	22	1	US-07-988-825-12	Sequence 12, Appl	235	4	57.1	70	2	US-10-004-860-1160	Sequence 1160, Ap
163	4	57.1	22	1	US-08-362-780-12	Sequence 12, Appl	236	4	57.1	71	2	US-09-270-767-59376	Sequence 59376, A
164	4	57.1	22	2	US-09-220-528-118	Sequence 118, App	237	4	57.1	71	2	US-09-583-110-5069	Sequence 5069, Ap
165	4	57.1	22	2	US-09-563-222C-87	Sequence 87, Appl	238	4	57.1	72	2	US-09-107-433-4759	Sequence 4759, Ap
166	4	57.1	22	2	US-09-563-222C-91	Sequence 91, Appl	239	4	57.1	72	2	US-09-248-796A-27260	Sequence 27260, A
167	4	57.1	22	2	US-09-563-222C-95	Sequence 95, Appl	240	4	57.1	73	2	US-09-513-998C-4967	Sequence 4967, Ap
168	4	57.1	22	2	US-09-563-222C-105	Sequence 105, App	241	4	57.1	73	2	US-09-248-796A-19552	Sequence 19552, A
169	4	57.1	22	2	US-08-478-684G-12	Sequence 12, Appl	242	4	57.1	74	2	US-09-248-796A-23440	Sequence 23440, A
170	4	57.1	28	2	US-09-471-276-819	Sequence 819, App	243	4	57.1	74	2	US-09-107-433-4363	Sequence 4363, App
171	4	57.1	28	2	US-10-001-887-123	Sequence 123, App	244	4	57.1	74	2	US-09-149-476-543	Sequence 543, App
172	4	57.1	32	2	US-09-242-890-5	Sequence 5, Appli	245	4	57.1	75	2		

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OM protein - protein search, using sw model

Run on: October 13, 2006, 01:14:17 ; Search time 40 Seconds
(without alignments)
16.838 Million cell updates/sec

Title: US-10-537-648-1

Perfect score: 7

Sequence: 1 YUTQPS 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 1

Total number of hits satisfying chosen parameters: 283334

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

PIR 80:*
1: pirl:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	85.7	290	2 A82236	pseudouridine synt
2	6	85.7	1375	2 T13822	frazzled gene prot
3	6	85.7	1526	2 T13823	frazzled gene prot
4	5	71.4	93	2 AF2346	hypothetical prote
5	5	71.4	135	2 G84469	probable glycine-r
6	5	71.4	157	2 T46440	hypothetical prote
7	5	71.4	177	2 G96794	probable calmoduli
8	5	71.4	193	2 T06972	hypothetical prote
9	5	71.4	206	2 H64022	hypothetical prote
10	5	71.4	214	2 S21969	19K zein precursor
11	5	71.4	220	2 S01838	nify protein - Kle
12	5	71.4	228	2 T49057	hypothetical prote
13	5	71.4	229	2 D83667	conserved hypothet
14	5	71.4	229	2 H83073	conserved hypothet
15	5	71.4	234	2 Z1ZM3	19K zein precursor
16	5	71.4	234	2 Z1ZMB1	19K zein precursor
17	5	71.4	234	2 S03417	19K zein precursor
18	5	71.4	239	2 T20603	hypothetical prote
19	5	71.4	249	2 J01981	lectin II - Scotch
20	5	71.4	253	2 T49820	hypothetical prote
21	5	71.4	258	2 H75436	conserved hypothet
22	5	71.4	284	2 S27843	homeotic protein s
23	5	71.4	291	2 D70080	transcription regu
24	5	71.4	295	2 A40587	probable transcrip
25	5	71.4	298	2 T52117	zinc finger protei
26	5	71.4	303	2 F81318	probable galactosy
27	5	71.4	303	2 T34112	hypothetical prote
28	5	71.4	310	2 E90867	hypothetical prote
29	5	71.4	310	2 D85751	hypothetical prote

30	5	71.4	310	2 B64882	conserved hypothet
31	5	71.4	318	2 G87342	hypothetical prote
32	5	71.4	331	2 AG0072	probable MCCA-fam1
33	5	71.4	333	2 A81399	hypothetical prote
34	5	71.4	334	2 D5097	YgiR protein - Eac
35	5	71.4	334	2 A88125	hypothetical prote
36	5	71.4	334	2 H85969	hypothetical prote
37	5	71.4	338	2 T47427	hypothetical prote
38	5	71.4	344	2 A80894	probable oxidoredu
39	5	71.4	348	2 D82252	Rnfp-related prote
40	5	71.4	379	2 JCS303	conserved hypothet
41	5	71.4	388	2 F64147	hypothetical prote
42	5	71.4	397	2 F27072	probable transamin
43	5	71.4	397	2 C86552	aspartate aminotra
44	5	71.4	402	2 B75297	dipeptidyl peptida
45	5	71.4	413	2 S73336	adhesin P1 precurs
46	5	71.4	426	2 T45800	UDP-N-acetylglucos
47	5	71.4	428	2 Q4ECAD	damX protein (arob
48	5	71.4	428	2 D86003	hypothetical prote
49	5	71.4	443	2 F91157	probable membrane
50	5	71.4	443	2 T10801	GDP dissociation i
51	5	71.4	450	2 D86717	hypothetical prote
52	5	71.4	455	2 H96797	hypothetical prote
53	5	71.4	460	2 A96555	unknown protein li
54	5	71.4	476	2 E83006	two-component resp
55	5	71.4	487	2 T29226	hypothetical prote
56	5	71.4	494	2 T42444	ID-myo-inositol-tr
57	5	71.4	517	2 E87613	pilus assembly pro
58	5	71.4	526	2 D96977	peptide chain rale
59	5	71.4	539	2 I49065	lymphoid-restrict
60	5	71.4	573	2 T00320	hypothetical prote
61	5	71.4	577	2 D91239	membrane protein l
62	5	71.4	577	2 A86087	hypothetical prote
63	5	71.4	577	2 F65202	hypothetical 66.6
64	5	71.4	613	2 A95552	oligoendopeptidase
65	5	71.4	634	1 S35574	transcription fact
66	5	71.4	645	2 T25824	hypothetical prote
67	5	71.4	654	2 T08600	hypothetical prote
68	5	71.4	690	2 H75469	conserved hypothet
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70	5	71.4	796	2 JCT355	peroxisome prolif
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74	5	71.4	928	1 RBHU	retinoblastoma-ass
75	5	71.4	939	2 C70876	hypothetical prote
76	5	71.4	968	2 F84693	hypothetical prote
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78	5	71.4	985	2 T27083	hypothetical prote
79	5	71.4	998	2 T30930	hypothetical prote
80	5	71.4	1009	2 T31081	cca3 protein - rat
81	5	71.4	1024	2 S38048	ubiquitin-protein
82	5	71.4	1097	2 T49187	hypothetical prote
83	5	71.4	1112	2 T30202	probable chitin sy
84	5	71.4	1113	2 S62904	calcium-regulated
85	5	71.4	1174	2 T43051	protein kinase C (
86	5	71.4	1175	2 JH0697	potassium channel
87	5	71.4	1184	2 A39800	calcium-activated
88	5	71.4	1184	2 I49017	calcium-activated
89	5	71.4	1189	2 S56852	hypothetical prote
90	5	71.4	1196	2 A48206	calcium-activated
91	5	71.4	1210	2 B64979	hypothetical 138.1
92	5	71.4	1226	2 E82328	s-methyltetrahydro
93	5	71.4	1467	2 T48162	hypothetical prote
94	5	71.4	4725	1 A44357	dysenin heavy chain
95	5	57.1	13	2 G61458	ig lamda chain V-
96	4	57.1	16	2 A45454	ankyrin-binding gl
97	4	57.1	21	2 B28835	ig heavy-chain V r
98	4	57.1	22	2 A37043	ig light chain, po
99	4	57.1	27	2 S00347	triacylglycerol li
100	4	57.1	27	2 B37043	ig heavy chain, po
101	4	57.1	27	2 A30323	amyloid protein AL
102	4	57.1	30	2 PL0189	ig light chain - s

103	4	57.1	30	2	S70341	napin large chain	176	4	57.1	100	2	E85677	unknown protein en
104	4	57.1	31	2	S77593	hypothetical prote	177	4	57.1	100	2	A98818	hypothetical prote
105	4	57.1	36	2	C37473	type I copoisomera	178	4	57.1	100	2	D87057	ig heavy chain V-D
106	4	57.1	39	2	E86636	50S ribosomal prot	179	4	57.1	101	2	S10387	ig heavy chain V-I
107	4	57.1	49	2	G82678	hypothetical prote	180	4	57.1	101	2	B47624	hypothetical prote
108	4	57.1	51	2	AB0546	hypothetical prote	181	4	57.1	101	2	T39075	ig heavy chain V-
109	4	57.1	54	2	AH1885	hypothetical prote	182	4	57.1	103	1	LIHUNM	ig heavy chain V-
110	4	57.1	57	2	A49111	POU homeodomain pr	183	4	57.1	103	2	S08462	ig heavy chain V r
111	4	57.1	61	1	DNVPBF	DNA-binding protei	184	4	57.1	103	2	S36067	ig lambda chain -
112	4	57.1	61	2	C82536	hypothetical prote	185	4	57.1	104	2	T04149	phytochrome rice
113	4	57.1	62	2	AD2912	hypothetical prote	186	4	57.1	104	2	S36064	ig lambda chain -
114	4	57.1	64	2	T25247	hypothetical prote	187	4	57.1	105	2	S44124	ig lambda chain V
115	4	57.1	64	2	B97177	hypothetical prote	188	4	57.1	105	2	S52680	ribosomal protein
116	4	57.1	64	2	H98033	hypothetical prote	189	4	57.1	106	1	L4HUBU	ig lambda chain V-
117	4	57.1	64	2	H98046	hypothetical prote	190	4	57.1	106	1	L4HUKN	ig lambda chain V-
118	4	57.1	67	2	F81853	probable transposa	191	4	57.1	106	1	L4HUKL	ig lambda chain V-
119	4	57.1	69	2	JH0348	T-cell receptor be	192	4	57.1	106	1	L4HUHL	ig lambda chain V-
120	4	57.1	70	2	PC2063	neurite outgrowth	193	4	57.1	107	1	L4HUX	ig lambda chain V-
121	4	57.1	70	2	AH2112	protein secretion	194	4	57.1	107	2	B46516	ig lambda chain V
122	4	57.1	72	1	O38CFS	hypothetical 8K pr	195	4	57.1	107	2	JH0347	T-cell receptor be
123	4	57.1	72	2	D85557	hypothetical prote	196	4	57.1	107	2	A82653	hypothetical prote
124	4	57.1	72	2	T12404	ATP synthetase sub	197	4	57.1	108	2	AI2341	hypothetical prote
125	4	57.1	72	2	T11887	ATP synthetase sub	198	4	57.1	108	2	JN0695	tributylin chlori
126	4	57.1	73	2	AI0290	hypothetical prote	199	4	57.1	109	1	LIHUBP	ig lambda chain V-
127	4	57.1	73	2	AH2157	hypothetical prote	200	4	57.1	109	1	LIHUBA	ig lambda chain V-
128	4	57.1	75	2	AB2497	hypothetical prote	201	4	57.1	109	1	L2HUBR	ig lambda chain V-
129	4	57.1	76	1	WSWL58	ES protein - human	202	4	57.1	109	2	S68171	ig lambda chain V-
130	4	57.1	76	2	T44556	hypothetical prote	203	4	57.1	110	1	L2HUS8	ig lambda chain V-
131	4	57.1	77	2	JQ1295	hypothetical 8.8K	204	4	57.1	110	2	S36258	ig lambda chain V-
132	4	57.1	78	2	B90778	hypothetical prote	205	4	57.1	110	2	S57428	ig light chain V-J
133	4	57.1	78	2	D70001	conserved hypothet	206	4	57.1	110	2	S57412	ig lambda chain V-
134	4	57.1	78	2	AD2386	hypothetical prote	207	4	57.1	110	2	S57408	ig lambda chain V-
135	4	57.1	80	2	F83467	regulatory protein	208	4	57.1	110	2	S57442	ig lambda chain V-
136	4	57.1	80	2	AD2345	hypothetical prote	209	4	57.1	110	2	S51149	hypothetical prote
137	4	57.1	81	2	I50975	MHC class II beta	210	4	57.1	110	2	G72597	hypothetical prote
138	4	57.1	81	2	I51144	MHC class II beta	211	4	57.1	111	1	LIHUNG	ig lambda chain V-
139	4	57.1	81	2	I51145	MHC class II beta	212	4	57.1	111	1	LIHUNW	ig lambda chain V-
140	4	57.1	84	2	D83940	hypothetical prote	213	4	57.1	111	1	LIHUNV	ig lambda chain V-
141	4	57.1	85	2	AF3548	transcription regu	214	4	57.1	111	1	LIHUVQ	ig lambda chain V-
142	4	57.1	86	2	E81144	hypothetical prote	215	4	57.1	111	1	L2HUBH	ig lambda chain V-
143	4	57.1	86	2	S15229	hypothetical prote	216	4	57.1	111	1	L2HUBO	ig lambda chain V-
144	4	57.1	87	2	AD3551	hypothetical prote	217	4	57.1	111	1	L2HUMC	ig lambda chain V-
145	4	57.1	89	1	WMV2RF	10K cell fusion pr	218	4	57.1	111	1	L2HUNI	ig lambda chain V-
146	4	57.1	89	2	E98123	transposase, uncha	219	4	57.1	111	1	L2HUTG	ig lambda chain V-
147	4	57.1	89	2	AG3394	hypothetical membr	220	4	57.1	111	1	L2HUTR	ig lambda chain V-
148	4	57.1	90	2	C83960	ribosomal protein	221	4	57.1	111	1	L2HUVL	ig lambda chain V-
149	4	57.1	91	2	C90867	hypothetical prote	222	4	57.1	111	1	L2HUNW	ig lambda chain V-
150	4	57.1	91	2	AG3691	conserved hypothet	223	4	57.1	111	1	L6HULT	ig lambda chain V-
151	4	57.1	91	2	C97473	damage-inducible p	224	4	57.1	111	1	L6HUST	ig lambda chain V-
152	4	57.1	92	2	D64039	hypothetical prote	225	4	57.1	111	1	L7HUMT	ig lambda chain V-
153	4	57.1	93	2	AC3330	hypothetical prote	226	4	57.1	111	2	S46396	ig lambda chain V-
154	4	57.1	94	2	S72864	hypothetical prote	227	4	57.1	111	2	S19671	ig lambda chain -
155	4	57.1	94	2	S72920	hypothetical prote	228	4	57.1	111	2	S71185	VL lambda protein
156	4	57.1	95	2	S36065	ig lambda chain -	229	4	57.1	111	2	S38499	ig lambda chain V1
157	4	57.1	96	2	S76170	hypothetical prote	230	4	57.1	111	2	S47009	ig lambda chain V
158	4	57.1	97	2	E53374	type IV preplin p	231	4	57.1	111	2	S36256	ig lambda chain V
159	4	57.1	97	2	I51216	ig light chain var	232	4	57.1	111	2	S36263	ig lambda chain V
160	4	57.1	97	2	S10385	ig heavy chain V r	233	4	57.1	111	2	S46397	ig lambda chain V
161	4	57.1	97	2	S07266	hypothetical prote	234	4	57.1	111	2	S19673	ig lambda chain V
162	4	57.1	98	2	S36068	ig lambda chain -	235	4	57.1	111	2	S36281	ig lambda chain V
163	4	57.1	98	2	S36047	ig lambda chain -	236	4	57.1	111	2	S36274	ig lambda chain V
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165	4	57.1	98	2	S36046	ig lambda chain -	238	4	57.1	111	2	S38497	ig lambda chain -
166	4	57.1	98	2	S36048	ig lambda chain -	239	4	57.1	112	1	LIHUBA	ig lambda chain V-
167	4	57.1	98	2	G69036	hypothetical prote	240	4	57.1	112	1	LIHUNM	ig lambda chain V-
168	4	57.1	99	2	S36053	ig lambda chain -	241	4	57.1	112	1	L2HUNG	ig lambda chain V-
169	4	57.1	99	2	S36055	ig lambda chain -	242	4	57.1	112	1	L6HUAR	ig lambda chain V-
170	4	57.1	99	2	S36057	ig lambda chain -	243	4	57.1	112	2	C44151	ig lambda chain V-
171	4	57.1	99	2	S36057	ig lambda chain -	244	4	57.1	112	2	S46395	ig lambda chain V-
172	4	57.1	99	2	S36058	ig lambda chain -	245	4	57.1	112	2	S44123	ig lambda chain V-
173	4	57.1	99	2	S36056	ig lambda chain -	246	4	57.1	112	2	D44151	ig lambda chain V
174	4	57.1	99	2	S36054	ig lambda chain -	247	4	57.1	112	2	A44151	ig lambda chain V
175	4	57.1	99	2	AD3031	hypothetical prote	248	4	57.1	112	2	S31515	ig lambda chain V

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OM protein - protein search, using sw model

Run on: October 13, 2006, 01:10:37 ; Search time 300 Seconds
(without alignments)
21.584 Million cell updates/sec

Title: US-10-537-648-1

Perfect score: 7

Sequence: 1 YLTQPS 7

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2849598 seqs, 92501592 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2849397

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : Uniprot 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	6	85.7	192	Q4SGH9	TETNG
4	6	85.7	216	Q6L17	PHOPR
5	6	85.7	227	P90610	TRIFO
6	6	85.7	230	Q42PBI	PSEU2
7	6	85.7	241	RLUE	VIBCH
8	6	85.7	362	1	RFPL RAT
9	6	85.7	453	Q4UFX1	THEAN
10	6	85.7	537	Q6NKA8	CORDI
11	6	85.7	546	Q3AVX9	SYNS9
12	6	85.7	562	Q349P1	RHOA
13	6	85.7	580	Q4SYV1	TETNG
14	6	85.7	693	Q4UH42	THEAN
15	6	85.7	698	Q4N8H3	THEPA
16	6	85.7	732	Q4N8H3	THEPA
17	6	85.7	740	Q4N8H3	THEPA
18	6	85.7	745	Q4N8H3	THEPA
19	6	85.7	877	Q54Y08	DICDI
20	6	85.7	1033	Q4H2B9	GIBZE
21	6	85.7	1136	Q6MEV2	PARUM
22	6	85.7	1375	Q8ML47	DRONE
23	6	85.7	1526	Q94538	DRONE
24	6	85.7	1526	Q94538	DRONE
25	5	71.4	13	Q9BDQ2	PANTR
26	5	71.4	45	Q3ME70	ANAVT
27	5	71.4	70	Q675B6	MOUSE
28	5	71.4	72	Q50370	MYCPAS
29	5	71.4	75	Q6SJC8	ROSOVIR
30	5	71.4	87	Q82V02	NITEU
31	5	71.4	91	Q322X6	SHIGBS

32	5	71.4	91	Q5N3U1	SYNP6
33	5	71.4	93	Q3MDN7	ANAVT
34	5	71.4	93	Q8YP75	ANASP
35	5	71.4	95	Q31OE7	SYNP7
36	5	71.4	95	Q3HB30	TRIER
37	5	71.4	99	Q8DMB0	SYNEL
38	5	71.4	107	Q2UV61	ASPOR
39	5	71.4	109	Q8CAF6	MOUSE
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43	5	71.4	117	Q38819	9HIV1
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45	5	71.4	128	Q8DHY7	SYNEL
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47	5	71.4	129	Q3S807	9HIV1
48	5	71.4	132	Q6NKA8	CORDI
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51	5	71.4	152	Q70KA6	9ACTO
52	5	71.4	155	Q7SF68	NEUCR
53	5	71.4	155	Q5LTV3	SILPO
54	5	71.4	149	Q27608	SULTO
55	5	71.4	149	Q27608	SULTO
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57	5	71.4	151	Q8NR47	CORGL
58	5	71.4	153	Q5BFY2	EMENI
59	5	71.4	155	Q76FB0	CVACA
60	5	71.4	155	Q44SE2	CHLLI
61	5	71.4	157	Q6J772	HUMAN
62	5	71.4	158	Q6MVK6	NEUCR
63	5	71.4	158	Q3L9Y2	RHOE4
64	5	71.4	162	Q2JMW3	9CVAN
65	5	71.4	162	Q2JXN5	9CVAN
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67	5	71.4	167	Q3CSL5	ALTAT
68	5	71.4	168	Q2YHN3	PLAMU
69	5	71.4	175	Q2XCT6	PSEPU
70	5	71.4	175	Q6WPM5	ECOLI
71	5	71.4	177	Q77040	BOMMO
72	5	71.4	177	Q8LBV6	ARATH
73	5	71.4	177	Q5SRE6	ARATH
74	5	71.4	178	Q5HN44	STAEQ
75	5	71.4	178	Q65DP9	BACLD
76	5	71.4	178	Q8CNP8	STAES
77	5	71.4	184	Q4Q240	LEIMA
78	5	71.4	184	Q45AP2	9BURK
79	5	71.4	184	Q4LTP9	9BURK
80	5	71.4	185	Q8N7H9	HUMAN
81	5	71.4	185	Q7MMJ3	VIBVU
82	5	71.4	185	Q8DG02	VIBVU
83	5	71.4	186	Q2SH37	9GAMM
84	5	71.4	188	Q5ONB0	ENTHI
85	5	71.4	188	Q2CWU8	MOUSE
86	5	71.4	190	Q5LN40	SILPO
87	5	71.4	191	KBR52	CHICK
88	5	71.4	191	KBR52	MOUSE
89	5	71.4	191	KBR52	MOUSE
90	5	71.4	191	Q4SAK0	TETNG
91	5	71.4	192	KBR52	BRARE
92	5	71.4	193	YCF21	CYAPA
93	5	71.4	196	Q2XOR0	9GAMM
94	5	71.4	196	Q2ZVC9	SHEPU
95	5	71.4	202	Q44983	CAEEL
96	5	71.4	202	Q61CUI	CAEEL
97	5	71.4	202	Q853R2	9CAUD
98	5	71.4	203	Q3J5P6	RHOE4
99	5	71.4	206	Y1244	HAELN
100	5	71.4	206	Q55J42	CRYNE
101	5	71.4	207	Q3FLZ1	9BURK
102	5	71.4	208	Q5B096	EMENI
103	5	71.4	208	Q30B81	9DEIN
104	5	71.4	208	Q41717	KINRA

Q5N3U1	synchococ
Q3MDN7	anabaena va
Q8YP75	anabaena sp
Q31OE7	synchococ
Q3HB30	trichodesmi
Q8DMB0	synchococ
Q2UV61	aspergillus
Q8CAF6	musculus
Q54XU9	dictyosteli
Q3CQ00	pseudosalter
Q5TG33	flamulina
Q38819	human immun
Q4S617	tetradon n
Q8DHY7	synchococ
Q9HAF6	homo sapien
Q3S807	human immun
Q6NKA8	corynebacte
Q5LTV3	arabidopsis
Q76FB0	gordonia we
Q7SF68	neurospora
Q5LTV3	silicibacte
Q76FB0	cyanidium c
Q44SE2	chlorobium
Q6J772	homo sapien
Q6MVK6	neurospora
Q3L9Y2	rhodococcus
Q2JMW3	cyanobacter
Q2JXN5	cyanobacter
Q7M7F7	gloeobacter
Q3CSL5	pseudosalter
Q2YHN3	plantago ma
Q2XCT6	pseudomonas
Q6WPM5	escherichia
Q77040	bombyx mori
Q8LBV6	arabidopsis
Q5SRE6	arabidopsis
Q5HN44	staphylococ
Q65DP9	bacillus li
Q8CNP8	staphylococ
Q4Q240	leishmania
Q45AP2	burkholderi
Q4LTP9	burkholderi
Q8N7H9	homo sapien
Q7MMJ3	vibrio vuln
Q8DG02	vibrio vuln
Q2SH37	hahella che
Q5ONB0	entamoeba h
Q2CWU8	mus musculus
Q5LN40	silicibacte
Q5JW6	gallus gall
Q9NYR9	homo sapien
Q55J42	mus musculus
Q4SAK0	tetradon n
Q6G12	brachydanio
P48358	cyanophora
Q2XOR0	shewanella
Q2ZVC9	shewanella
Q44983	caenorhabdi
Q61CUI	caenorhabdi
Q853R2	mycobacteri
Q3J5P6	rhodobacter
P44134	haemophilus
Q55J42	cryptococcu
Q3FLZ1	rhodoferrax
Q5B096	aspergillus
Q30B81	thermus sp.
Q41717	kineococcus

105	5	71.4	209	2	077039	BOMMO	077039	bombyx mori	178	5	71.4	279	2	088AQ3	PSESM	088AQ3	pseudomonas	179	5	71.4	282	2	09RD75	STRCO	09RD75	streptomyces
106	5	71.4	209	2	051227	ENTHI	051227	entamoeba h	179	5	71.4	283	2	09RD75	STRCO	09RD75	streptomyces	180	5	71.4	283	2	05RH54	BRARE	05RH54	brachydanio
107	5	71.4	209	2	030XA4	DESDG	030XA4	desulfobact	180	5	71.4	284	2	05RH54	BRARE	05RH54	brachydanio	181	5	71.4	284	2	1SMOXS	SCMA	1SMOXS	schistosoma
108	5	71.4	211	2	0320C0	SHIBS	0320C0	shigella bo	181	5	71.4	284	2	1SMOXS	SCMA	1SMOXS	schistosoma	182	5	71.4	285	2	05AT53	EMENI	05AT53	aspergillus
109	5	71.4	212	2	0518A7	ENTHI	0518A7	entamoeba h	182	5	71.4	285	2	05AT53	EMENI	05AT53	aspergillus	183	5	71.4	285	2	04AGR9	9CHLB	04AGR9	cholorobium
110	5	71.4	212	2	07QY16	GIALA	07QY16	giardia lam	183	5	71.4	285	2	04AGR9	9CHLB	04AGR9	cholorobium	184	5	71.4	287	2	03IC24	PSEHT	03IC24	pseudocalter
111	5	71.4	213	2	032828	PELUD	032828	pelodictyon	184	5	71.4	287	2	03IC24	PSEHT	03IC24	pseudocalter	185	5	71.4	288	2	08X0N6	NEUCR	08X0N6	neurospora
112	5	71.4	214	2	041877	MAIZE	041877	zea mays (m	185	5	71.4	288	2	08X0N6	NEUCR	08X0N6	neurospora	186	5	71.4	289	2	048KA0	PSE14	048KA0	pseudomonas
113	5	71.4	215	1	Y1650	HAEDU	Y1650	haemophilus	186	5	71.4	289	2	048KA0	PSE14	048KA0	pseudomonas	187	5	71.4	289	2	073EP9	BACCI	073EP9	bacillus ce
114	5	71.4	216	2	05FQZ3	GLUOX	05FQZ3	gluconobact	187	5	71.4	289	2	073EP9	BACCI	073EP9	bacillus ce	188	5	71.4	289	2	08JG31	CHICK	08JG31	gallus gall
115	5	71.4	218	2	03RV01	RALME	03RV01	ralstonia m	188	5	71.4	289	2	08JG31	CHICK	08JG31	gallus gall	189	5	71.4	290	2	04HUM5	GIBZE	04HUM5	gibberella
116	5	71.4	218	2	04VOT4	BACCC	04VOT4	bacillus ce	189	5	71.4	290	2	04HUM5	GIBZE	04HUM5	gibberella	190	5	71.4	290	2	03GBD3	9FIRM	03GBD3	syntrophomo
117	5	71.4	219	2	09VQJ8	DROME	09VQJ8	drosophila	190	5	71.4	290	2	03GBD3	9FIRM	03GBD3	syntrophomo	191	5	71.4	290	2	04ZU27	PSEU2	04ZU27	pseudomonas
118	5	71.4	222	2	05B8V3	EMENI	05B8V3	aspergillus	191	5	71.4	290	2	04ZU27	PSEU2	04ZU27	pseudomonas	192	5	71.4	291	1	YXJ07	BACSU	YXJ07	bacillus su
119	5	71.4	223	2	07NE50	GLOVI	07NE50	gloeobacter	192	5	71.4	291	1	YXJ07	BACSU	YXJ07	bacillus su	193	5	71.4	292	2	0845T3	VIBVU	0845T3	vibrio vuln
120	5	71.4	224	1	SNZ2	HUMAN	SNZ2	homo sapien	193	5	71.4	292	2	0845T3	VIBVU	0845T3	vibrio vuln	194	5	71.4	292	2	08DSB1	VIBVU	08DSB1	vibrio vuln
121	5	71.4	227	2	08BNX8	MOUSE	08BNX8	mus musculus	194	5	71.4	292	2	08DSB1	VIBVU	08DSB1	vibrio vuln	195	5	71.4	292	2	08E861	SHEUN	08E861	shewanella
122	5	71.4	228	2	09LXY4	ARATH	09LXY4	arabidopsis	195	5	71.4	292	2	08E861	SHEUN	08E861	shewanella	196	5	71.4	292	2	09PS77	CHICK	09PS77	gallus gall
123	5	71.4	229	1	ISPD	NEIMA	ISPD	neisseria m	196	5	71.4	293	2	09PS77	CHICK	09PS77	gallus gall	197	5	71.4	293	2	05ZP99	9DELT	05ZP99	angiococcus
124	5	71.4	229	1	ISPD	NEIMA	ISPD	neisseria m	197	5	71.4	293	2	05ZP99	9DELT	05ZP99	angiococcus	198	5	71.4	294	2	02X611	9GAMM	02X611	shewanella
125	5	71.4	229	1	NIEY	KLEPN	NIEY	klebsiella	198	5	71.4	294	2	02X611	9GAMM	02X611	shewanella	199	5	71.4	294	2	02ZQ82	SHEPU	02ZQ82	syntrophoba
126	5	71.4	229	2	Q5F829	NEIG1	Q5F829	neisseria g	199	5	71.4	294	2	02ZQ82	SHEPU	02ZQ82	syntrophoba	200	5	71.4	294	2	03N3N5	9DELT	03N3N5	myxococcus
127	5	71.4	230	2	Q3KGM8	PSEPF	Q3KGM8	pseudomonas	200	5	71.4	295	1	RPSC	MYXXX	RPSC	myxococcus	201	5	71.4	295	1	08J2Q9	GIBMO	08J2Q9	gibberella
128	5	71.4	230	2	Q4KXG5	PSEPF5	Q4KXG5	pseudomonas	201	5	71.4	295	1	08J2Q9	GIBMO	08J2Q9	gibberella	202	5	71.4	295	1	07VVS9	BORPE	07VVS9	bordetella
129	5	71.4	230	2	Q3V3H7	MOUSE	Q3V3H7	mus musculus	202	5	71.4	295	1	07VVS9	BORPE	07VVS9	bordetella	203	5	71.4	295	2	07W7A4	BORPE	07W7A4	bordetella
130	5	71.4	234	1	ZEAL	MAIZE	ZEAL	zea mays (m	203	5	71.4	295	2	07W7A4	BORPE	07W7A4	bordetella	204	5	71.4	295	2	07WKP1	BORBR	07WKP1	bordetella
131	5	71.4	234	1	ZEAL	MAIZE	ZEAL	zea mays (m	204	5	71.4	295	2	07WKP1	BORBR	07WKP1	bordetella	205	5	71.4	295	2	04K9M0	PSEF5	04K9M0	pseudomonas
132	5	71.4	234	1	ZEAS	MAIZE	ZEAS	zea mays (m	205	5	71.4	295	2	04K9M0	PSEF5	04K9M0	pseudomonas	206	5	71.4	295	2	06BMJ9	DEBHA	06BMJ9	debaromyces
133	5	71.4	234	2	Q946V6	MAIZE	Q946V6	zea mays (m	206	5	71.4	295	2	06BMJ9	DEBHA	06BMJ9	debaromyces	207	5	71.4	297	2	064936	ARATH	064936	arabidopsis
134	5	71.4	234	2	Q4AXJ9	9BURK	Q4AXJ9	polaromonas	207	5	71.4	297	2	064936	ARATH	064936	arabidopsis	208	5	71.4	298	2	07MC82	VIBVU	07MC82	vibrio vuln
135	5	71.4	235	2	067E24	9TELE	067E24	beryll splen	208	5	71.4	298	2	07MC82	VIBVU	07MC82	vibrio vuln	209	5	71.4	298	2	04HSD9	9DEIO	04HSD9	deinococcus
136	5	71.4	237	2	Q31KM9	PSEHT	Q31KM9	pseudocalter	209	5	71.4	298	2	04HSD9	9DEIO	04HSD9	deinococcus	210	5	71.4	299	2	03K3Y5	PSEPF	03K3Y5	pseudomonas
137	5	71.4	239	2	Q9XVA0	CABEL	Q9XVA0	caenorhabdi	210	5	71.4	299	2	03K3Y5	PSEPF	03K3Y5	pseudomonas	211	5	71.4	299	2	RNH3	CHUCV	RNH3	chlamydomo
138	5	71.4	240	2	Q4CHF5	CLOTM	Q4CHF5	clostridium	211	5	71.4	300	1	RNH3	CHUCV	RNH3	chlamydomo	212	5	71.4	300	2	Q2W9G6	MAGSA	Q2W9G6	magnetocospir
139	5	71.4	242	2	Q2JUS5	9ACTO	Q2JUS5	frankia sp.	212	5	71.4	300	2	Q2W9G6	MAGSA	Q2W9G6	magnetocospir	213	5	71.4	300	2	Q3C6U8	9CLOT	Q3C6U8	alkaliphilu
140	5	71.4	246	1	Q88YR6	LACPL	Q88YR6	lactobacill	213	5	71.4	300	2	Q3C6U8	9CLOT	Q3C6U8	alkaliphilu	214	5	71.4	300	2	05HVN7	CAMJR	05HVN7	campylobact
141	5	71.4	248	1	LEC2	CVTSC	LEC2	cytiscus eco	214	5	71.4	300	2	05HVN7	CAMJR	05HVN7	campylobact	215	5	71.4	301	2	02S842	NITEU	02S842	nitrosomona
142	5	71.4	248	2	Q4H9K4	9DEIO	Q4H9K4	deinococcus	215	5	71.4	301	2	02S842	NITEU	02S842	nitrosomona	216	5	71.4	302	2	050M40	ENTHI	050M40	entamoeba h
143	5	71.4	249	2	Q890D4	LACPL	Q890D4	lactobacill	216	5	71.4	302	2	050M40	ENTHI	050M40	entamoeba h	217	5	71.4	302	2	087189	VIBPA	087189	vibrio para
144	5	71.4	249	2	Q89SD5	BRAJA	Q89SD5	bradyrhizob	217	5	71.4	302	2	087189	VIBPA	087189	vibrio para	218	5	71.4	303	2	07F191	ORYSA	07F191	oryza sativ
145	5	71.4	250	2	Q4DLB2	TRYCR	Q4DLB2	trypanosoma	218	5	71.4	303	2	07F191	ORYSA	07F191	oryza sativ	219	5	71.4	303	2	09PNF5	CAMJE	09PNF5	campylobact
146	5	71.4	250	2	Q517R9	ENTHI	Q517R9	entamoeba h	219	5	71.4	303	2	09PNF5	CAMJE	09PNF5	campylobact	220	5	71.4	304	2	02T2C7	BURTH	02T2C7	burkholderi
147	5	71.4	251	2	Q2SYPB8	BURTH	Q2SYPB8	burkholderi	220	5	71.4	304	2	02T2C7	BURTH	02T2C7	burkholderi	221	5	71.4	304	2	082S45	NITEU	082S45	nitrosomona
148	5	71.4	252	2	Q2U0E8	ASPOR	Q2U0E8	aspergillus	221	5	71.4	304	2	082S45	NITEU	082S45	nitrosomona	222	5	71.4	306	2	09VGJ4	DROME	09VGJ4	drosophila
149	5	71.4	252	2	Q4DEC9	TRYCR	Q4DEC9	trypanosoma	222	5	71.4	306	2	09VGJ4	DROME	09VGJ4	drosophila	223	5	71.4	306	2	Q83LA7	SHIFL	Q83LA7	shigella fl
150	5	71.4	254	1	SCYBG	HUMAN	SCYBG	homo sapien	223	5	71.4	306	2	Q83LA7	SHIFL	Q83LA7	shigella fl	224	5	71.4	307	2	Q3XNH2	9PROT	Q3XNH2	magnetococc
151	5	71.4	254	2	Q7Q9R3	ANOAG	Q7Q9R3	anopheles g	224	5	71.4	310	1	YCJY	ECOLI	YCJY	escherichia	225	5	71.4	310	2	05QPJ1	HUMAN	05QPJ1	homo saplen
152	5	71.4	256	2	Q8XYM8	RALSO	Q8XYM8	ralstonia s	225	5	71.4	310	2	05QPJ1	HUMAN	05QPJ1	homo saplen	226	5	71.4	310	2	054G80	DICDI	054G80	dictyosteli
153	5	71.4	258	2	Q7VIA4	HELHP	Q7VIA4	helicobacte	226	5	71.4	310	2	054G80	DICDI	054G80	dictyosteli	227	5	71.4	311	2	04FXB8	LEIMA	04FXB8	leishmania
154	5	71.4	258	2	Q8PGV5	SYNEL	Q8PGV5	synecococc	227	5	71.4	311	2	04FXB8	LEIMA	04FXB8	leishmania	228	5	71.4	311	2	04LY78	9BURK	04LY78	burkholderi
155	5	71.4	258	2	Q8RVC8	DEIRA	Q8RVC8	deinococcus	228	5	71.4	311	2	04LY78	9BURK	04LY78	burkholderi	229	5	71.4	311	2	03Q346	BURS3	03Q346	silicibacte
156	5	71.4	260	2	Q8KKW8	RHLET	Q8KKW8	rhizobium e	229	5	71.4	311	2	03Q346	BURS3	03Q346	silicibacte	230	5	71.4	312	2	Q3QV37	9RHOB	Q3QV37	thiobacillu
157	5	71.4	260	2	Q6DBF6	ERWCT	Q6DBF6	erwinia car	230	5	71.4	312	2	Q3QV37	9RHOB	Q3QV37	thiobacillu	231	5	71.4	313	2	09ZH27	THIDE	09ZH27	thiobacillu
158	5	71.4	261	2	Q9N3Z9	CABEL	Q9N3Z9	caenorhabdi	231	5	71.4	313	2	09ZH27	THIDE	09ZH27	thiobacillu	232	5	71.4	313	2	Q3SFM8	THIDA	Q3SFM8	synecococc
159	5	71.4	261	2	Q5HKP																					

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: October 13, 2006, 01:00:06 ; Search time 41 Seconds
(without alignments)
16.427 Million cell updates/sec

Title: US-10-537-648-1
Perfect score: 37
Sequence: 1 YLTQPS 7

Scoring table: BLOSUM62
Gapop 10.0 , Capext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	89.2	331	2 F69025	ATP phosphoribosyl
2	32	86.5	264	2 B71448	hypothetical prote
3	32	86.5	539	2 I49065	lymphoid-restrict
4	32	86.5	921	4 A33718	retinoblastoma pro
5	32	86.5	928	1 RBHU	retinoblastoma-as
6	31	83.8	294	2 S27843	homeotic protein s
7	31	83.8	538	2 B83625	probable gamma-glu
8	30	81.1	290	2 A82326	pseudouridine synt
9	30	81.1	528	2 G70055	probable choline d
10	30	81.1	645	2 T25824	hypothetical prote
11	30	81.1	705	2 B82044	guanosine-3',5'-bi
12	30	81.1	980	2 T49570	hypothetical prote
13	30	81.1	1205	2 C84848	hypothetical prote
14	30	81.1	1375	2 T13822	frazzled gene prot
15	30	81.1	1483	2 T19751	hypothetical prote
16	30	81.1	1526	2 T13823	frazzled gene prot
17	29	78.4	214	2 S21969	19K zein precursor
18	29	78.4	229	2 T33141	hypothetical prote
19	29	78.4	234	1 ZIZN3	19K zein precursor
20	29	78.4	234	1 ZIZMB1	19K zein precursor
21	29	78.4	234	2 S03417	19K zein precursor
22	29	78.4	248	2 AB1941	hypothetical prote
23	29	78.4	263	2 A54543	beta-lactamase (EC
24	29	78.4	263	2 S23929	beta-lactamase (EC
25	29	78.4	291	2 S42075	beta-lactamase (EC
26	29	78.4	294	2 S19006	beta-lactamase (EC
27	29	78.4	327	2 T34562	G protein pathway
28	29	78.4	382	1 MFN241	matrix protein - s
29	29	78.4	402	2 B75297	dipeptidyl peptida

30	29	78.4	450	2 D86717	hypothetical prote
31	29	78.4	460	2 A36555	unknown protein [i
32	29	78.4	466	2 S75657	coproporphyrinogen
33	29	78.4	578	2 S74578	probable flavoprot
34	29	78.4	612	2 E64820	probable oligopept
35	29	78.4	612	2 D90742	hypothetical prote
36	29	78.4	612	2 G85592	hypothetical prote
37	29	78.4	613	2 T09105	holocytochrome c-t
38	29	78.4	637	2 S75772	hypothetical prote
39	29	78.4	1883	2 G82875	hypothetical prote
40	28	75.7	75	2 S36422	retrovirus-related
41	28	75.7	81	2 T15040	RNA-directed DNA p
42	28	75.7	81	2 T10743	RNA-directed DNA p
43	28	75.7	89	2 C47759	retrovirus-related
44	28	75.7	138	2 A29679	thyrotropin beta c
45	28	75.7	146	2 S36970	hypothetical prote
46	28	75.7	157	2 T36140	hypothetical prote
47	28	75.7	193	2 T66972	hypothetical prote
48	28	75.7	206	2 H64022	hypothetical prote
49	28	75.7	239	2 T20603	hypothetical prote
50	28	75.7	241	2 A04048	4-diphosphocytidyl
51	28	75.7	245	2 G64471	cell division prot
52	28	75.7	253	2 T49820	hypothetical prote
53	28	75.7	291	2 T70080	transcription regu
54	28	75.7	292	2 T03085	ribonuclease homol
55	28	75.7	303	2 F81318	probable galactosy
56	28	75.7	303	2 T34112	hypothetical prote
57	28	75.7	308	2 AC1867	hypothetical prote
58	28	75.7	310	2 E90867	hypothetical prote
59	28	75.7	310	2 D85751	hypothetical prote
60	28	75.7	310	2 B64882	conserved hypothet
61	28	75.7	318	2 G87342	hypothetical prote
62	28	75.7	333	2 A81399	hypothetical prote
63	28	75.7	338	2 T47427	hypothetical prote
64	28	75.7	426	2 T45800	UDP-N-acetylglucos
65	28	75.7	443	2 T10801	GDP dissociation i
66	28	75.7	515	1 IQMCL	replication initia
67	28	75.7	517	2 E87613	pilus assembly pro
68	28	75.7	547	2 JC7539	beta-glucosidase (
69	28	75.7	573	2 T00320	hypothetical prote
70	28	75.7	577	2 D91239	membrane protein [
71	28	75.7	577	2 A86087	hypothetical prote
72	28	75.7	577	2 F52202	hypothetical 66.6
73	28	75.7	632	2 H70339	NADH2 dehydrogenas
74	28	75.7	661	2 T46364	hypothetical prote
75	28	75.7	722	2 T26297	hypothetical prote
76	28	75.7	769	2 F85077	probable transposo
77	28	75.7	815	2 B30843	glutenin high mole
78	28	75.7	815	2 JN0689	glutenin, high-mol
79	28	75.7	830	2 S15720	glutenin high mole
80	28	75.7	838	1 E8WTHW	glutenin, high mol
81	28	75.7	848	2 S02262	glutenin high mole
82	28	75.7	853	2 T46347	hypothetical prote
83	28	75.7	874	2 I64095	alanine-tRNA ligas
84	28	75.7	919	2 S45298	retinoblastoma-ass
85	28	75.7	925	2 T00781	hypothetical prote
86	28	75.7	939	2 C70876	hypothetical prote
87	28	75.7	950	2 E64135	oxoglutarate dehyd
88	28	75.7	964	2 T01860	reverse transcript
89	28	75.7	985	2 T27083	hypothetical prote
90	28	75.7	990	2 JC7878	fucokinase (EC 2.7
91	28	75.7	1024	2 S38048	ubiquitin-protein
92	28	75.7	1113	2 S62904	calcium-regulated
93	28	75.7	1139	2 A49370	BLA-associated cyc
94	28	75.7	1175	2 JH0697	potassium channel
95	28	75.7	1184	2 A39800	calcium-activated
96	28	75.7	1184	2 I49017	calcium-activated
97	28	75.7	1196	2 A48206	calcium-activated
98	28	75.7	1199	2 S20969	Na+/Ca2+,K+-exchan
99	28	75.7	1447	2 F82909	hypothetical prote
100	28	75.7	2241	2 S09811	hypothetical prote
101	28	75.7	7829	2 T15789	hypothetical prote
102	28	75.7	9376	2 T14593	synergomycin synth

103	27	73.0	81	2	T03723	reverse transcript	176	27	73.0	1176	2	I58345	protein tyrosine p
104	27	73.0	92	2	T03665	reverse transcript	177	27	73.0	1200	2	E84473	probable retroelem
105	27	73.0	92	2	T03617	retrovirus-related	178	27	73.0	1307	2	H84467	probable retroelem
106	27	73.0	93	2	AF2346	hypothetical prote	179	27	73.0	1490	2	T30550	ABC transport prot
107	27	73.0	107	2	A82653	hypothetical prote	180	27	73.0	1706	2	B75633	probable RNA helic
108	27	73.0	111	2	T49549	hypothetical prote	181	27	73.0	2186	2	T13169	tiggrin - fruit fl
109	27	73.0	121	2	S24660	hypothetical prote	182	27	73.0	2201	2	AH0095	probable sideropho
110	27	73.0	140	2	PH0134	Ig heavy chain v r	183	27	73.0	2440	2	S39162	transcription coac
111	27	73.0	141	2	T31118	Ig lambda chain pr	184	27	73.0	2441	2	S39161	CREB-binding prote
112	27	73.0	141	2	T36810	msHP protein - Vib	185	27	73.0	3796	2	T18514	lysosomal traffick
113	27	73.0	143	2	B82328	hypothetical prote	186	27	73.0	387	2	T28402	ORF MSV241 leucine
114	27	73.0	154	2	S39873	hypothetical prote	187	26	70.3	11	2	S21127	precocin methyltr
115	27	73.0	180	2	JU0149	hypothetical prote	188	26	70.3	51	2	T31672	homeobox protein -
116	27	73.0	182	2	T16472	zein protein - mai	189	26	70.3	62	2	AD2912	hypothetical prote
117	27	73.0	194	2	S19141	hypothetical prote	190	26	70.3	86	2	E81144	hypothetical prote
118	27	73.0	195	2	S77152	beta-coixin, 17K,	191	26	70.3	88	2	I47758	retrovirus-related
119	27	73.0	195	2	AF2347	hypothetical prote	192	26	70.3	89	2	T06321	reverse transcript
120	27	73.0	197	2	S72585	ygrp protein - Myc	193	26	70.3	89	2	T06283	reverse transcript
121	27	73.0	205	2	I64155	hypothetical prote	194	26	70.3	89	2	A47759	retrovirus-related
122	27	73.0	213	2	AD2728	hypothetical prote	195	26	70.3	97	2	S31094	hypothetical prote
123	27	73.0	213	2	S67818	GumB protein - Xan	196	26	70.3	99	2	S36057	Ig lambda chain -
124	27	73.0	214	2	E82942	glucose inhibited	197	26	70.3	109	1	L2HUBR	Ig lambda chain V-
125	27	73.0	224	2	T47401	hypothetical prote	198	26	70.3	110	1	L2HUB8	Ig lambda chain V-
126	27	73.0	225	2	E97509	hypothetical prote	199	26	70.3	110	2	S57412	Ig lambda chain V-
127	27	73.0	274	2	AC2299	cobalt transport A	200	26	70.3	111	1	L2HUBH	Ig lambda chain V-
128	27	73.0	298	2	J01207	attachment protein	201	26	70.3	111	1	L2HUTR	Ig lambda chain V-
129	27	73.0	300	2	B71079	hypothetical prote	202	26	70.3	113	2	T39875	hypothetical prote
130	27	73.0	331	2	T22042	hypothetical prote	203	26	70.3	123	2	H81694	inclusion membrane
131	27	73.0	339	2	S61240	hypothetical prote	204	26	70.3	135	2	G84469	probable glycine-r
132	27	73.0	343	2	F70587	probable hrcA prot	205	26	70.3	148	2	S57402	ynes protein - Bac
133	27	73.0	343	2	F83896	hypothetical prote	206	26	70.3	177	2	G96794	probable calmoduli
134	27	73.0	343	2	H85986	probable heat-indu	207	26	70.3	189	2	A32840	hypothetical 22K p
135	27	73.0	348	1	Z1BFP1	Gene I protein - p	208	26	70.3	193	1	S75588	dCTP deaminase (EC
136	27	73.0	348	1	Z1BFPD	Gene I protein - p	209	26	70.3	198	2	F84284	sulfite oxidase ho
137	27	73.0	348	1	Z1BPM3	Gene I protein - p	210	26	70.3	198	2	A97395	hypothetical prote
138	27	73.0	361	2	AH2434	hypothetical prote	211	26	70.3	211	2	AE1977	conserved hypotet
139	27	73.0	397	2	F72072	probable transamin	212	26	70.3	212	2	F86545	amidotransferase [
140	27	73.0	397	2	C86552	aspartate aminotra	213	26	70.3	212	2	F72077	hypothetical prote
141	27	73.0	408	2	H87193	probable FAD-linka	214	26	70.3	215	2	A12093	hypothetical prote
142	27	73.0	426	2	F71220	hypothetical prote	215	26	70.3	216	2	S89130	signal peptidase I
143	27	73.0	426	2	G75187	probable trehalose	216	26	70.3	218	2	B64365	Ig lambda chain (D
144	27	73.0	428	1	Q4ECAD	damX protein (arob	217	26	70.3	220	2	S01838	hypothetical prote
145	27	73.0	428	2	D86003	hypothetical prote	218	26	70.3	228	2	T49057	hypothetical prote
146	27	73.0	428	2	F91157	probable membrane	219	26	70.3	229	2	D81867	conserved hypotet
147	27	73.0	430	2	AE1803	sugar binding prot	220	26	70.3	229	2	H81073	conserved hypotet
148	27	73.0	430	2	AF1429	sugar binding prot	221	26	70.3	229	2	JQ1981	lectin II - Scotch
149	27	73.0	433	2	A99398	hypothetical prote	222	26	70.3	249	2	H75436	conserved hypotet
150	27	73.0	434	2	G82184	glycerol-3-phospha	223	26	70.3	258	2	AG2215	hypothetical prote
151	27	73.0	453	2	AG0353	probable RNA-bind	224	26	70.3	272	2	AG2215	prolyl aminopeptid
152	27	73.0	453	2	G96695	hypothetical prote	225	26	70.3	275	2	AB1284	conserved hypotet
153	27	73.0	461	2	D87971	protein Y43F8A.2 [226	26	70.3	276	2	F72342	hypothetical prote
154	27	73.0	469	2	A45728	membrane protein r	227	26	70.3	282	2	T21222	probable zinc-fing
155	27	73.0	491	2	T26994	phal protein precu	228	26	70.3	284	2	A84682	beta-lactamase (EC
156	27	73.0	492	2	S54536	probable membrane	229	26	70.3	291	2	JP0074	lyser family transc
157	27	73.0	502	2	T26851	hypothetical prote	230	26	70.3	292	2	D86859	probable transcrip
158	27	73.0	503	2	G95251	conserved hypotet	231	26	70.3	295	2	A40587	transcription regu
159	27	73.0	503	2	D98116	hypothetical prote	232	26	70.3	296	2	H83988	zinc finger protai
160	27	73.0	538	2	A48692	pyruvate dehydrog	233	26	70.3	298	2	T52117	transcription regu
161	27	73.0	592	2	T21536	hypothetical prote	234	26	70.3	303	2	F70356	hypothetical prote
162	27	73.0	607	2	G97780	hypothetical prote	235	26	70.3	306	2	H89791	capsular polysacch
163	27	73.0	705	2	C84406	hypothetical prote	236	26	70.3	307	2	T44638	hypothetical prote
164	27	73.0	805	2	HA1938	sucrose synthase [237	26	70.3	309	2	AH2927	algM1 (AB011415) [
165	27	73.0	835	2	T47521	respiratory burst	238	26	70.3	309	2	G98354	transcription regu
166	27	73.0	883	2	T08648	phycobilisome link	239	26	70.3	316	2	S75062	hypothetical prote
167	27	73.0	884	2	T40690	hypothetical prote	240	26	70.3	317	1	C71239	hypothetical prote
168	27	73.0	885	2	S67660	hypothetical prote	241	26	70.3	324	2	T06970	beta lactamase pre
169	27	73.0	891	2	T40503	protein kinase kin	242	26	70.3	326	2	A70455	probable transposa
170	27	73.0	891	2	A38903	protein kinase 1 -	243	26	70.3	328	2	T14989	probable transpos
171	27	73.0	926	2	B84642	hypothetical prote	244	26	70.3	328	2	AH0002	conserved hypotet
172	27	73.0	961	2	T01167	hypothetical prote	245	26	70.3	331	2	AG0072	probable MOCA-fam
173	27	73.0	973	2	T21463	hypothetical prote	246	26	70.3	334	2	T50816	probable transcrip
174	27	73.0	1021	2	T42634	connectin/titin -	247	26	70.3	334	2	D65097	YgjR protein - Bac
175	27	73.0	1060	2	AI0201	beta-galactosidase	248	26	70.3	334	2	A98125	hypothetical prote

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OM protein - protein search, using sw model

Run on: October 13, 2006, 01:05:31 ; Search time 187 Seconds
(without alignments)
17.340 Million cell updates/sec

Title: US-10-537-648-1

Perfect score: 37

Sequence: 1 YLTQPS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

Published Applications AA Main:*

- 1: /EMC_Celella_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /EMC_Celella_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 3: /EMC_Celella_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 4: /EMC_Celella_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 5: /EMC_Celella_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 6: /EMC_Celella_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	89.2	87	4	US-10-425-115-291176
2	33	89.2	119	4	US-10-425-115-224207
3	33	89.2	251	4	US-10-319-799-68
4	33	89.2	331	4	US-10-369-493-1104
5	33	89.2	415	5	US-10-501-282-2354
6	33	89.2	503	5	US-10-501-282-2356
7	33	89.2	717	5	US-10-501-282-2358
8	32	86.5	264	5	US-10-739-930-6322
9	32	86.5	781	3	US-09-469-522-33
10	32	86.5	815	5	US-10-732-923-15103
11	22	86.5	816	3	US-09-469-522-4
12	32	86.5	832	3	US-09-469-522-35
13	32	86.5	851	3	US-09-469-522-33
14	32	86.5	851	3	US-09-469-522-39
15	32	86.5	869	3	US-09-469-522-47
16	32	86.5	871	3	US-09-469-522-49
17	32	86.5	874	3	US-09-469-522-31
18	32	86.5	882	5	US-10-732-923-15123
19	32	86.5	895	3	US-09-469-522-29
20	32	86.5	897	3	US-09-469-522-41
21	32	86.5	899	5	US-10-732-923-15104
22	32	86.5	921	5	US-10-492-901-11
23	32	86.5	921	5	US-10-732-923-15102
24	32	86.5	928	3	US-09-758-007-3
25	32	86.5	928	3	US-09-860-211-8
26	32	86.5	928	3	US-09-469-522-2
27	32	86.5	928	3	US-09-469-522-51

28	86.5	928	3	US-09-860-286-8	Sequence 8, Appli
29	86.5	928	3	US-09-860-286-8	Sequence 8, Appli
30	86.5	928	4	US-10-028-726-2	Sequence 2, Appli
31	86.5	928	4	US-10-442-754-8	Sequence 8, Appli
32	86.5	928	4	US-10-441-510-8	Sequence 8, Appli
33	86.5	928	4	US-10-408-765A-49	Sequence 49, Appli
34	86.5	928	5	US-10-766-363-8	Sequence 8, Appli
35	86.5	928	5	US-10-732-923-15124	Sequence 15124, A
36	86.5	928	5	US-10-732-923-15125	Sequence 15125, A
37	86.5	928	5	US-10-732-923-15126	Sequence 15126, A
38	86.5	928	5	US-10-732-923-15127	Sequence 15127, A
39	86.5	928	5	US-10-442-754-8	Sequence 8, Appli
40	86.5	928	6	US-11-130-594-8	Sequence 8, Appli
41	86.5	928	6	US-11-201-801-8	Sequence 8, Appli
42	83.8	81	4	US-10-156-761-15087	Sequence 15087, A
43	83.8	128	5	US-10-450-763-32634	Sequence 32634, A
44	83.8	228	4	US-10-767-701-32911	Sequence 32911, A
45	83.8	339	4	US-10-282-122A-45042	Sequence 45042, A
46	83.8	562	4	US-10-032-585-7639	Sequence 7639, Ap
47	83.8	1047	6	US-11-097-143-29241	Sequence 29241, A
48	81.1	95	4	US-10-424-599-268773	Sequence 268773, A
49	81.1	106	4	US-10-425-115-339436	Sequence 339436, A
50	81.1	162	4	US-10-425-114-45986	Sequence 45986, A
51	81.1	175	4	US-10-425-115-197546	Sequence 197546, A
52	81.1	341	5	US-10-501-282-822	Sequence 822, App
53	81.1	345	5	US-10-501-282-824	Sequence 824, App
54	81.1	437	4	US-10-425-114-43857	Sequence 43857, A
55	81.1	488	4	US-10-425-115-263721	Sequence 263721, A
56	81.1	528	3	US-09-712-363-194	Sequence 194, App
57	81.1	528	4	US-10-282-122A-62830	Sequence 62830, A
58	81.1	528	4	US-10-282-122A-64520	Sequence 64520, A
59	81.1	538	4	US-10-230-026-18	Sequence 18, Appl
60	81.1	538	5	US-10-486-307-18	Sequence 18, Appl
61	81.1	705	4	US-10-282-122A-77556	Sequence 77556, A
62	81.1	738	5	US-10-741-849-7213	Sequence 7213, Ap
63	81.1	1375	3	US-09-800-602-66	Sequence 66, Appl
64	81.1	1375	3	US-09-800-198-55	Sequence 55, Appl
65	81.1	1526	6	US-11-097-143-18609	Sequence 18609, A
66	78.4	10	3	US-09-827-345-8	Sequence 8, Appli
67	78.4	10	4	US-10-227-616-47	Sequence 47, Appl
68	78.4	10	6	US-11-220-407-8	Sequence 8, Appli
69	78.4	39	5	US-10-472-533-402	Sequence 402, App
70	78.4	40	4	US-10-195-730-194	Sequence 194, App
71	78.4	40	4	US-10-799-747-194	Sequence 194, App
72	78.4	40	5	US-10-979-183-194	Sequence 194, App
73	78.4	49	4	US-10-264-049-4292	Sequence 4292, Ap
74	78.4	55	4	US-10-425-115-311628	Sequence 311628, A
75	78.4	66	4	US-10-424-599-209887	Sequence 209887, A
76	78.4	66	4	US-10-425-115-188144	Sequence 188144, A
77	78.4	67	4	US-10-425-115-211727	Sequence 211727, A
78	78.4	67	4	US-10-425-115-325848	Sequence 325848, A
79	78.4	69	4	US-10-425-115-337261	Sequence 337261, A
80	78.4	71	4	US-10-425-115-260249	Sequence 260249, A
81	78.4	72	4	US-10-425-115-282526	Sequence 282526, A
82	78.4	73	4	US-10-425-115-251146	Sequence 251146, A
83	78.4	74	4	US-10-425-115-200807	Sequence 200807, A
84	78.4	76	4	US-10-425-115-302677	Sequence 302677, A
85	78.4	77	4	US-10-242-355-580	Sequence 580, App
86	78.4	77	4	US-10-425-115-236263	Sequence 236263, A
87	78.4	78	4	US-10-425-115-247760	Sequence 247760, A
88	78.4	81	5	US-10-450-763-37171	Sequence 37171, A
89	78.4	83	4	US-10-425-115-305630	Sequence 305630, A
90	78.4	94	4	US-10-425-115-329601	Sequence 329601, A
91	78.4	97	4	US-10-425-115-318800	Sequence 318800, A
92	78.4	99	5	US-10-450-763-53129	Sequence 53129, A
93	78.4	103	4	US-10-425-115-237989	Sequence 237989, A
94	78.4	108	4	US-10-425-115-353035	Sequence 353035, A
95	78.4	111	5	US-10-450-763-50208	Sequence 50208, A
96	78.4	112	4	US-10-425-115-353801	Sequence 353801, A
97	78.4	115	4	US-10-425-115-227440	Sequence 227440, A
98	78.4	117	4	US-10-425-115-335802	Sequence 335802, A
99	78.4	117	4	US-10-425-115-336635	Sequence 336635, A
100	78.4	118	4	US-10-425-115-296283	Sequence 296283, A

101	29	78.4	119	4	US-10-425-115-302847	Sequence 302847,	174	29	78.4	224	4	US-10-002-967A-162	Sequence 162, App
102	29	78.4	125	4	US-10-425-115-333983	Sequence 333983,	175	29	78.4	224	4	US-10-017-083A-162	Sequence 162, App
103	29	78.4	126	4	US-10-425-115-336605	Sequence 336605,	176	29	78.4	224	4	US-10-145-128A-162	Sequence 162, App
104	29	78.4	126	4	US-10-425-115-336667	Sequence 336667,	177	29	78.4	224	4	US-10-017-191A-162	Sequence 162, App
105	29	78.4	127	4	US-10-425-115-283489	Sequence 283489,	178	29	78.4	224	4	US-10-143-028A-162	Sequence 162, App
106	29	78.4	129	4	US-10-425-115-201349	Sequence 201349,	179	29	78.4	224	4	US-10-143-029A-162	Sequence 162, App
107	29	78.4	134	4	US-10-425-115-50827	Sequence 50827, A	180	29	78.4	224	4	US-10-145-089A-162	Sequence 162, App
108	29	78.4	134	4	US-10-425-115-336688	Sequence 336688,	181	29	78.4	224	4	US-10-165-067A-162	Sequence 162, App
109	29	78.4	134	4	US-10-425-115-364360	Sequence 364360,	182	29	78.4	224	4	US-10-145-017A-162	Sequence 162, App
110	29	78.4	135	4	US-10-425-115-364360	Sequence 364360,	183	29	78.4	224	4	US-10-164-728A-162	Sequence 162, App
111	29	78.4	136	4	US-10-425-115-325604	Sequence 325604,	184	29	78.4	224	4	US-10-013-926A-162	Sequence 162, App
112	29	78.4	137	4	US-10-425-115-242287	Sequence 242287,	185	29	78.4	224	4	US-10-165-247A-162	Sequence 162, App
113	29	78.4	139	4	US-10-425-115-232139	Sequence 232139,	186	29	78.4	224	4	US-10-145-124A-162	Sequence 162, App
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 12, 2006, 21:41:10 ; Search time 148 Seconds

(without alignments)
132.500 Million cell updates/sec

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Fgapop 60.0 , Fgapext 7.0
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Searched: 2395520 seqs, 934235491 residues

Word size: 1

Total number of hits satisfying chosen parameters: 4785881

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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126	5	71.4	111	7	US-11-434-137-1141	Sequence 1141, Ap	C 199	5	71.4	420	8	US-11-266-748A-215081	Sequence 215081, A
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128	5	71.4	133	8	US-11-266-748A-4113110	Sequence 4113110, Ap	C 201	5	71.4	422	8	US-11-266-748A-419364	Sequence 419364, A
129	5	71.4	151	8	US-11-266-748A-378139	Sequence 378139, Ap	C 202	5	71.4	423	8	US-11-266-748A-375454	Sequence 375454, A
130	5	71.4	151	8	US-11-266-748A-461518	Sequence 461518, Ap	C 203	5	71.4	423	8	US-11-266-748A-458833	Sequence 458833, A
131	5	71.4	154	8	US-11-266-748A-413862	Sequence 413862, Ap	C 204	5	71.4	425	6	US-10-834-268-201	Sequence 201, App
132	5	71.4	156	7	US-11-244-330A-2426	Sequence 2426, Ap	C 205	5	71.4	425	6	US-10-834-268-930	Sequence 930, App
133	5	71.4	159	8	US-11-266-748A-264229	Sequence 264229, Ap	C 206	5	71.4	425	8	US-11-266-748A-374167	Sequence 374167, A
134	5	71.4	159	8	US-11-266-748A-324746	Sequence 324746, Ap	C 207	5	71.4	425	8	US-11-266-748A-457546	Sequence 457546, A
135	5	71.4	170	7	US-10-284-444-1275	Sequence 1275, Ap	C 208	5	71.4	426	7	US-11-244-330A-5086	Sequence 5086, Ap
136	5	71.4	201	6	US-10-284-444-733	Sequence 733, App	C 209	5	71.4	429	6	US-10-517-420-15	Sequence 15, Appl
137	5	71.4	201	6	US-10-284-444-1449	Sequence 1449, Ap	C 210	5	71.4	430	8	US-11-266-748A-377620	Sequence 377620, A
138	5	71.4	201	6	US-10-284-444-3584	Sequence 3584, Ap	C 211	5	71.4	430	8	US-11-266-748A-460999	Sequence 460999, A
139	5	71.4	201	6	US-10-284-444-5919	Sequence 5919, Ap	C 212	5	71.4	431	8	US-11-266-748A-103021	Sequence 103021, A
140	5	71.4	201	6	US-10-284-444-21280	Sequence 21280, A	C 213	5	71.4	431	8	US-11-266-748A-155832	Sequence 155832, A
141	5	71.4	201	6	US-10-284-444-26445	Sequence 26445, A	C 214	5	71.4	432	8	US-11-266-748A-229798	Sequence 229798, A
142	5	71.4	201	6	US-10-284-444-26910	Sequence 26910, A	C 215	5	71.4	435	6	US-10-517-420-23	Sequence 23, Appl
143	5	71.4	201	6	US-10-284-444-26966	Sequence 26966, A	C 216	5	71.4	436	7	US-11-177-646-193	Sequence 193, App
144	5	71.4	201	6	US-10-284-444-27690	Sequence 27690, A	C 217	5	71.4	436	8	US-11-266-748A-178818	Sequence 178818, A
145	5	71.4	216	8	US-11-266-748A-414075	Sequence 414075, Ap	C 218	5	71.4	448	8	US-11-266-748A-60439	Sequence 60439, A
146	5	71.4	231	8	US-11-266-748A-231265	Sequence 231265, Ap	C 219	5	71.4	450	8	US-11-183-218-43	Sequence 43, Appl
147	5	71.4	247	7	US-11-244-330A-1255	Sequence 1255, Ap	C 220	5	71.4	450	8	US-11-169-140-5	Sequence 5, Appl1
148	5	71.4	254	7	US-11-244-330A-1118	Sequence 1118, Ap	C 221	5	71.4	452	8	US-11-266-748A-259587	Sequence 259587, A
149	5	71.4	254	7	US-11-244-330A-1101	Sequence 1101, Ap	C 222	5	71.4	452	8	US-11-266-748A-278954	Sequence 278954, A
150	5	71.4	258	7	US-11-244-330A-1244	Sequence 1244, Ap	C 223	5	71.4	452	8	US-11-266-748A-306194	Sequence 306194, A
151	5	71.4	260	7	US-11-244-330A-1106	Sequence 1106, Ap	C 224	5	71.4	452	8	US-11-266-748A-320104	Sequence 320104, A
152	5	71.4	260	7	US-11-244-330A-5097	Sequence 5097, Ap	C 225	5	71.4	457	8	US-11-266-748A-36278	Sequence 36278, A
153	5	71.4	261	8	US-11-266-748A-168984	Sequence 168984, Ap	C 226	5	71.4	457	8	US-11-266-748A-91459	Sequence 91459, A

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 12, 2006, 20:39:59 ; Search time 2564 Seconds

(without alignments)
261.875 Million cell updates/sec

Title: US-10-537-648-1

Perfect score: 37

Sequence: 1 YLTQPS 7

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Command line parameters: -DEV-xlp

-MODE=frame+pn.model -DEV-xlp
-O=/abss/ABSSWEB/spool/US10537648/runat_12102006_151424_15036/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=1000
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=100 -MODE=LOCAL
-OUTFWT=PCO -NORM=EXT -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abss03p
-USER=US10537648@CGN_1_1_8348@runat_12102006_151424_15036 -NCPU=6 -ICPU=3
-NO WMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPEXT=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*
1: gb_env.*
2: gb_pat.*
3: gb_ph.*
4: gb_pl.*
5: gb_pr.*
6: gb_ro.*
7: gb_sts.*
8: gb_sy.*
9: gb_un.*
10: gb_vi.*
11: gb_ov.*
12: gb_hcg.*
13: gb_in.*
14: gb_om.*
15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	37 100.0	21	2	CQ828007 Sequence
2	37 100.0	2000	2	AX656858 Sequence
3	37 100.0	44681	13	AC092520 Ciona sav

4	37	100.0	69037	6	AC003949	AC003949 Mus muscu
5	37	100.0	92797	5	AF038458	AF038458 Homo sapi
6	37	100.0	99489	12	AC084843	AC084843 Homo sapi
7	37	100.0	103836	6	AC125670	AC125670 Rattus no
8	37	100.0	105538	4	OSJN00043	AL606612 Rytza sat
9	37	100.0	110000	4	AF08207_428	Continuation (429
10	37	100.0	110000	4	AF08210_007	Continuation (8 of
11	37	100.0	112833	12	AC153744	AC153744 Ornithorh
12	37	100.0	130225	12	AC177977	AC177977 Strongylo
13	37	100.0	131761	12	AC164507	AC164507 Loxodonta
14	37	100.0	135924	14	AC163264	AC163264 Rhinoloph
15	37	100.0	137877	12	AC167095	AC167095 Sorex ara
16	37	100.0	139969	12	AC170718	AC170718 Atelerix
17	37	100.0	144819	12	AC173446	AC173446 Atelerix
18	37	100.0	148743	11	EX324154	EX324154 Zebrafish
19	37	100.0	151772	6	AC109294	AC109294 Mus muscu
20	37	100.0	155624	5	AC027058	AC027058 Homo sapi
21	37	100.0	165228	5	CNS01DWS	AL138479 Human chr
22	37	100.0	166758	12	AC173466	AC173466 Sorex ara
23	37	100.0	167388	12	AC157445	AC157445 Sus scrof
24	37	100.0	170875	6	AC154429	AC154429 Mus muscu
25	37	100.0	172427	5	AC161282	AC161282 Pan trogl
26	37	100.0	172853	5	AC084361	AC084361 Homo sapi
27	37	100.0	173555	4	AP003277	AP003277 Rytza sat
28	37	100.0	179085	5	AC175825	AC175825 Pan trogl
29	37	100.0	184106	12	AC144662	AC144662 Rattus no
30	37	100.0	188181	5	AC073879	AC073879 Homo sapi
31	37	100.0	192769	11	EX571945	EX571945 Zebrafish
32	37	100.0	196040	12	EX936414	EX936414 Danio rer
33	37	100.0	198138	6	AC108443	AC108443 Mus muscu
34	37	100.0	198392	11	CR383678	CR383678 Zebrafish
35	37	100.0	198694	6	EX072557	EX072557 Mouse DNA
36	37	100.0	203905	12	AC166470	AC166470 Bos tauru
37	37	100.0	205476	12	AC139733	AC139733 Sus scrof
38	37	100.0	211542	6	AC126275	AC126275 Mus muscu
39	37	100.0	212186	6	AC132237	AC132237 Mus muscu
40	37	100.0	212556	6	AC127294	AC127294 Mus muscu
41	37	100.0	215691	12	AC162334	AC162334 Bos tauru
42	37	100.0	216921	12	EX322658	EX322658 Mus muscu
43	37	100.0	218094	12	AC094408	AC094408 Rattus no
44	37	100.0	219298	6	AC161378	AC161378 Mus muscu
45	37	100.0	222489	12	AC117015	AC117015 Rattus no
46	37	100.0	225617	12	AC110849	AC110849 Rattus no
47	37	100.0	231580	12	AC136817	AC136817 Rattus no
48	37	100.0	232346	6	CR974489	CR974489 Mouse DNA
49	37	100.0	235024	12	AC120681	AC120681 Rattus no
50	37	100.0	235183	12	AC079427	AC079427 Mus muscu
51	37	100.0	236235	12	AC120331	AC120331 Rattus no
52	37	100.0	239915	6	AC124977	AC124977 Mus muscu
53	37	100.0	240181	12	AC098105	AC098105 Rattus no
54	37	100.0	241481	12	AC160175	AC160175 Bos tauru
55	37	100.0	245996	12	AC096933	AC096933 Rattus no
56	37	100.0	259204	12	AC095370	AC095370 Rattus no
57	37	100.0	271699	12	AC095812	AC095812 Rattus no
58	37	100.0	282933	12	AC122970	AC122970 Rattus no
59	37	100.0	295904	12	AC119509	AC119509 Rattus no
60	35	94.6	2018	4	BT013437	BT013437 Lycopersi
61	35	94.6	2180	15	AV206432	AV206432 Shigella
62	35	94.6	16098	2	AX680082	AX680082 Sequence
63	35	94.6	37026	5	CNS00YVF	AL096808 Homo sapi
64	35	94.6	55700	5	AL583824	AL583824 Human DNA
65	35	94.6	107000	5	AC069417	AC069417 Homo sapi
66	35	94.6	118402	12	AC182438	AC182438 Zea mays
67	35	94.6	126697	15	CP000037	CP000037 Shigella
68	35	94.6	131716	12	AC025833	AC025833 Homo sapi
69	35	94.6	136694	15	AY879342	AY879342 Shigella
70	35	94.6	137248	6	AC124678	AC124678 Mus muscu
71	35	94.6	140306	5	HG1068F16	AL023913 Human DNA
72	35	94.6	142152	12	AC139658	AC139658 Rattus no
73	35	94.6	147700	12	AC162733	AC162733 Loxodonta
74	35	94.6	154684	5	AC093763	AC093763 Homo sapi
75	35	94.6	165216	12	AC079092	AC079092 Homo sapi
76	35	94.6	166238	12	AC019280	AC019280 Homo sapi

77	35	94.6	168700	12	AC009115	AC009115 Homo sapi	C 150	34	91.9	145796	4	AC130598	AC130598 Oryza sat
78	35	94.6	173911	5	AL354992	AL354992 Human DNA	C 151	34	91.9	146492	4	AC136223	AC136223 Oryza sat
79	35	94.6	177738	5	AC021593	AC021593 Homo sapi	C 152	34	91.9	146958	12	CT573437	CT573437 Pan trogl
80	35	94.6	182726	15	CP000035	CP000035 Shigella	C 153	34	91.9	148720	12	BX327319	BX327319 Mus muscu
81	35	94.6	185321	12	AC173169	AC173169 Bos tauru	C 154	34	91.9	151772	6	AC109294	AC109294 Mus muscu
82	35	94.6	190171	12	AC149270	AC149270 Zea mays	C 155	34	91.9	151863	12	AC179790	AC179790 Strongylo
83	35	94.6	201661	12	AC171488	AC171488 Bos tauru	C 156	34	91.9	152476	12	AP001869	AP001869 Homo sapi
84	35	94.6	202678	12	AC135648	AC135648 Rattus no	C 157	34	91.9	152951	5	AC026371	AC026371 Homo sapi
85	35	94.6	213494	15	SPWR100	SPWR100 Shigella	C 158	34	91.9	153178	12	AC100929	AC100929 Homo sapi
86	35	94.6	214396	15	CP000039	CP000039 Shigella	C 159	34	91.9	153713	6	AC119889	AC119889 Mus muscu
87	35	94.6	218596	11	CR751234	CR751234 Zebrafish	C 160	34	91.9	154959	6	AL662881	AL662881 Mouse DNA
88	35	94.6	221493	12	AC098143	AC098143 Rattus no	C 161	34	91.9	155410	12	AC179303	AC179303 Strongylo
89	35	94.6	221618	15	AF386526	AF386526 Shigella	C 162	34	91.9	155451	12	AC067774	AC067774 Homo sapi
90	35	94.6	221851	15	AF348706	AF348706 Shigella	C 163	34	91.9	155547	6	AC132595	AC132595 Mus muscu
91	35	94.6	225039	12	AC111941	AC111941 Rattus no	C 164	34	91.9	155691	12	AC023214	AC023214 Homo sapi
92	35	94.6	228546	6	AL807234	AL807234 Mouse DNA	C 165	34	91.9	156500	12	CR792441	CR792441 Danio rer
93	35	94.6	235671	12	AC130022	AC130022 Rattus no	C 166	34	91.9	157652	5	AC135851	AC135851 Homo sapi
94	35	94.6	236372	12	AC098033	AC098033 Rattus no	C 167	34	91.9	158039	6	AL663110	AL663110 Mouse DNA
95	35	94.6	238075	12	AC127907	AC127907 Rattus no	C 168	34	91.9	160799	12	AC177126	AC177126 Strongylo
96	35	94.6	257222	12	AC108271	AC108271 Rattus no	C 169	34	91.9	161154	6	AC116868	AC116868 Mus muscu
97	35	94.6	263390	12	AC172070	AC172070 Bos tauru	C 170	34	91.9	164715	12	AC161706	AC161706 Orolemur
98	35	94.6	264661	12	AC103215	AC103215 Rattus no	C 171	34	91.9	166166	5	AC079380	AC079380 Homo sapi
99	34	91.9	376	2	CQ441235	CQ441235 Sequence	C 172	34	91.9	166930	11	AC146690	AC146690 Gaasterost
100	34	91.9	410	4	AB016143	AB016143 Solanum m	C 173	34	91.9	166976	12	AC034274	AC034274 Homo sapi
101	34	91.9	622	7	BV354507	BV354507 S231P686R	C 174	34	91.9	167589	12	AC034274	AC034274 Strongylo
102	34	91.9	1981	2	AR671031	AR671031 Sequence	C 175	34	91.9	168025	12	AC024364	AC024364 Homo sapi
103	34	91.9	1981	5	AK056166	AK056166 Homo sapi	C 176	34	91.9	168197	6	AC137511	AC137511 Mus muscu
104	34	91.9	2000	2	AX509675	AX509675 Sequence	C 177	34	91.9	168293	12	AC018397	AC018397 Homo sapi
105	34	91.9	2000	2	AX652380	AX652380 Sequence	C 178	34	91.9	168443	12	AC137940	AC137940 Mus muscu
106	34	91.9	2229	7	BV178520	BV178520 sqm10107	C 179	34	91.9	169243	5	AC104816	AC104816 Homo sapi
107	34	91.9	2422	5	BC063873	BC063873 Homo sapi	C 180	34	91.9	169310	6	AC119259	AC119259 Mus muscu
108	34	91.9	2448	2	AX684874	AX684874 Sequence	C 181	34	91.9	171790	6	BX537331	BX537331 Mouse DNA
109	34	91.9	2959	5	AK092222	AK092222 Homo sapi	C 182	34	91.9	172476	5	AC007736	AC007736 Homo sapi
110	34	91.9	3221	11	BC084750	BC084750 Xenopus l	C 183	34	91.9	172507	5	AC092960	AC092960 Homo sapi
111	34	91.9	3740	4	USMTO1	USMTO1 Ustilago ma	C 184	34	91.9	172549	12	AC027519	AC027519 Homo sapi
112	34	91.9	3951	4	AX099660	AX099660 Arabidops	C 185	34	91.9	172613	5	AC113398	AC113398 Homo sapi
113	34	91.9	5379	2	AX345232	AX345232 Arabidops	C 186	34	91.9	174923	12	AC023350	AC023350 Homo sapi
114	34	91.9	14096	15	AF084104	AF084104 Bacillus	C 187	34	91.9	175419	12	AC177128	AC177128 Strongylo
115	34	91.9	14293	15	AE003950	AE003950 Xylella f	C 188	34	91.9	175737	12	AC147487	AC147487 Orolemur
116	34	91.9	18120	4	NCOA	NCOA Neurospora	C 189	34	91.9	176692	12	AC164601	AC164601 Mus muscu
117	34	91.9	18215	13	U97552	U97552 Caenorhabdi	C 190	34	91.9	177771	6	AC115949	AC115949 Mus muscu
118	34	91.9	36020	13	CEC12D8	CEC12D8 Caenorhabdi	C 191	34	91.9	178011	6	AC129572	AC129572 Mus muscu
119	34	91.9	45962	12	AC006498	AC006498 Neurospor	C 192	34	91.9	179888	6	AC102287	AC102287 Mus muscu
120	34	91.9	52089	12	CR352281	CR352281 Homo sapi	C 193	34	91.9	179968	12	AC140813	AC140813 Homo sapi
121	34	91.9	57073	15	BA000038_18	Continuation (19 o	C 194	34	91.9	180001	5	AC112196	AC112196 Homo sapi
122	34	91.9	59652	12	AC137082	AC137082 Danio rer	C 195	34	91.9	181555	12	AC128628	AC128628 Rattus no
123	34	91.9	69126	5	AL354752	AL354752 Human DNA	C 196	34	91.9	181589	11	AC146544	AC146544 Gaasterost
124	34	91.9	84432	4	AC005850	AC005850 Human DNA	C 197	34	91.9	183218	6	AC132440	AC132440 Mus muscu
125	34	91.9	85745	11	BX936340	BX936340 Zebrafish	C 198	34	91.9	183544	6	AC102132	AC102132 Mus muscu
126	34	91.9	85745	12	AC136769	AC136769 Homo sapi	C 199	34	91.9	189246	12	AC177713	AC177713 Strongylo
127	34	91.9	85745	12	AP008104	AP008104 Lotus cor	C 200	34	91.9	189263	12	AC176030	AC176030 Strongylo
128	34	91.9	95954	12	AC177384	AC177384 Strongylo	C 201	34	91.9	190504	12	AC172252	AC172252 Bos tauru
129	34	91.9	95972	12	AL353639	AL353639 Human DNA	C 202	34	91.9	190840	6	AC159688	AC159688 Mus muscu
130	34	91.9	103822	6	AL845327	AL845327 Mouse DNA	C 203	34	91.9	191494	6	AL591488	AL591488 Mouse DNA
131	34	91.9	108176	6	CR382126_01	Continuation (2 of	C 204	34	91.9	192636	12	AC177237	AC177237 Strongylo
132	34	91.9	110000	4	AP008211_016	Continuation (17 o	C 205	34	91.9	193489	6	AC158347	AC158347 Mus muscu
133	34	91.9	110000	4	AP008211_081	Continuation (82 o	C 206	34	91.9	193785	12	AC118517	AC118517 Rattus no
134	34	91.9	110000	15	AE015451_38	Continuation (39 o	C 207	34	91.9	193857	12	AC109541	AC109541 Rattus no
135	34	91.9	110000	15	AE016796_12	Continuation (13 o	C 208	34	91.9	194156	12	AC182058	AC182058 Bos tauru
136	34	91.9	110000	15	BA000038_17	Continuation (18 o	C 209	34	91.9	195733	6	AL928960	AL928960 Mouse DNA
137	34	91.9	118955	5	AC068274	AC068274 Homo sapi	C 210	34	91.9	196152	5	AC021242	AC021242 Homo sapi
138	34	91.9	124074	5	HS112520	HS112520 Homo sapi	C 211	34	91.9	196567	12	AC178103	AC178103 Strongylo
139	34	91.9	128898	12	AC147464	AC147464 Orolemur	C 212	34	91.9	196916	6	AC164402	AC164402 Mus muscu
140	34	91.9	133202	5	AL139182	AL139182 Human DNA	C 213	34	91.9	197896	11	AC146543	AC146543 Gaasterost
141	34	91.9	134928	12	AC168497	AC168497 Strongylo	C 214	34	91.9	197906	6	AC153422	AC153422 Mus muscu
142	34	91.9	135301	12	AC175999	AC175999 Strongylo	C 215	34	91.9	200910	6	AC083946	AC083946 Mus muscu
143	34	91.9	137385	12	AC113357	AC113357 Homo sapi	C 216	34	91.9	201282	6	AC132450	AC132450 Mus muscu
144	34	91.9	137385	12	AC151647	AC151647 Daasyus n	C 217	34	91.9	201625	12	AC012144	AC012144 Homo sapi
145	34	91.9	137690	12	AC151647	AC151647 Daasyus n	C 218	34	91.9	202686	11	AC146539	AC146539 Gaasterost
146	34	91.9	138302	5	AC108060	AC108060 Homo sapi	C 219	34	91.9	202686	11	AC146539	AC146539 Gaasterost
147	34	91.9	139977	12	CR456630	CR456630 Danio rer	C 220	34	91.9	203246	12	AC162046	AC162046 Bos tauru
148	34	91.9	142740	6	AC103674	AC103674 Mus muscu	C 221	34	91.9	203422	6	AL713863	AL713863 Mouse DNA
149	34	91.9	143111	12	CR626923	CR626923 Danio rer	C 222	34	91.9	204899	5	AC117457	AC117457 Homo sapi

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 12, 2006, 21:08:36 ; Search time 3103 Seconds

(without alignments)
189.221 Million cell updates/sec

Title: US-10-537-648-1

Perfect score: 7

Sequence: 1 YLTQPS 7

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

Searched: 48236798 seqs, 2795965780 residues

Word size: 1

Total number of hits satisfying chosen parameters: 96457779

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:

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-DB=EST -QFMT=fastap -SUFFIX=p2n.olig.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=1000
-DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=100 -MODE=LOCAL -OUTFMT=ptc
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs02h
-USER=US10537648-CCGN_1_6323-@runat_12102006_151454_15415 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
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Database :

EST:*

1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_est7:*
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8: gb_est9:*
9: gb_est10:*
10: gb_est11:*
11: gb_est12:*
12: gb_est13:*
13: gb_est14:*
14: gb_est15:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	100.0	288	7	BB358863
2	7	100.0	304	6	AK200728
3	7	100.0	320	12	CE853641
4	7	100.0	331	11	A2240574

5	7	100.0	346	9	DA534392
6	7	100.0	392	13	CZ638826
7	7	100.0	413	11	AQ252207
8	7	100.0	458	14	DE130155
9	7	100.0	475	14	CR176637
10	7	100.0	494	14	CR192824
11	7	100.0	509	11	AQ464802
12	7	100.0	511	14	CR260251
13	7	100.0	515	14	CR251702
14	7	100.0	571	2	BJ838064
15	7	100.0	620	12	BZ879825
16	7	100.0	633	2	BZ826782
17	7	100.0	692	12	BZ921378
18	7	100.0	726	11	AQ077211
19	7	100.0	743	2	BJ830318
20	7	100.0	755	14	CR149426
21	7	100.0	769	14	AG494285
22	7	100.0	790	11	BH598970
23	7	100.0	797	14	BX966213
24	7	100.0	798	14	CR130680
25	7	100.0	801	14	CT047189
26	7	100.0	809	11	BH064279
27	7	100.0	815	13	CL831140
28	7	100.0	826	12	CG674428
29	7	100.0	826	14	AG866816
30	7	100.0	854	12	CC541008
31	7	100.0	859	12	CG818959
32	7	100.0	870	14	AG896133
33	7	100.0	987	14	CNS047BX
34	6	85.7	87	12	CG490574
35	6	85.7	100	8	CK211855
36	6	85.7	120	3	BM725400
37	6	85.7	125	3	BM677827
38	6	85.7	126	8	CN457244
39	6	85.7	134	7	BF440592
40	6	85.7	136	10	DV839525
41	6	85.7	144	2	BG463666
42	6	85.7	149	5	CK452301
43	6	85.7	149	5	CK453358
44	6	85.7	149	5	CK463686
45	6	85.7	149	5	CK464041
46	6	85.7	149	7	AW103591
47	6	85.7	149	9	DN120722
48	6	85.7	149	9	DN121075
49	6	85.7	150	13	CL631860
50	6	85.7	152	12	CE424767
51	6	85.7	162	3	EU034130
52	6	85.7	170	11	AZ218234
53	6	85.7	175	10	DM167722
54	6	85.7	178	7	BF395118
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56	6	85.7	181	2	BF922055
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58	6	85.7	186	1	AI300247
59	6	85.7	188	2	BM194624
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61	6	85.7	195	1	AI283482
62	6	85.7	195	7	BB584501
63	6	85.7	198	1	AI381735
64	6	85.7	199	1	AJ705322
65	6	85.7	199	4	BY418866
66	6	85.7	201	1	AL376300
67	6	85.7	206	1	AI349368
68	6	85.7	212	5	CF107239
69	6	85.7	212	10	DY161690
70	6	85.7	214	1	AA977165
71	6	85.7	214	2	BG223350
72	6	85.7	216	11	BH490823
73	6	85.7	219	1	AI675377
74	6	85.7	219	1	AI970690
75	6	85.7	219	11	BH100187
76	6	85.7	221	1	AA105635
77	6	85.7	222	1	AA980984

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CZ638826	OM_Ba018
AQ252207	HS_3184_A
DE130155	Oryzias_1
CR176637	Reverse_s
CR192824	Reverse_s
AQ464802	HS_5105_B
CR260251	Reverse_s
CR251702	Reverse_s
BJ838064	BJ838064
BZ879825	CH240_293
BZ826782	BJ826782
BZ921378	CH240_119
AQ077211	CIT-HSP-2
BJ830318	BJ830318
CR149426	Reverse_s
AG494285	Mus muscu
BH598970	BOGVELITF
BX966213	Reverse_s
CR130680	Reverse_s
CT047189	Sus scrofa
BH064279	RPCI-24-3
CL831140	OR_CB005
CG674428	Try2160_c
AG866816	Oryza sat
CC541008	CH240_421
CG818959	SOYCD72TH
AG896133	Oryza sat
AL277782	Tetraodon
CG490574	OST27777
CK211855	MNS15676
BM725400	UI-E-EJO-
BM677827	UI-E-EJO-
CN457244	UI-M-HPO-
BF440592	BS2900010
DV839525	LB01125_C
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CK452301	907909 MA
CK453358	909061 MA
CK463686	934608 MA
CK464041	934992 MA
AW103591	xe79910.x
DN120722	1120763 M
DN121075	1121147 M
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CE424767	tigr-gss-
EU034130	QHU3D02.y
AZ218234	Sheared D
DM167722	CLVY612.b
BF395118	UI-R-CMO-
BH059583	RPCI-24-9
BF922055	CM2-NT017
AW772133	hm7h08.x
AI300247	qm70e11.x
BM194624	TCAAP3Q13
BZ784599	PUGCZ82TD
AI283482	gh94c06.x
BB584501	BB584501
AI381735	te42e08.x
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AA977165	oq25a06.s
BG223350	na179h05_
BH490823	BOGBX08TF
AI675377	wb98f04.x
AI970690	wr19d05.x
BH100187	RPCI-24-3
AA105635	mm8e08.r
AA980984	vx55a01.r

C 78	222	14	DU486164	DU486164	109842109	C 151	6	85.7	310	10	DW164859
C 79	225	2	B1003642	B1003642	PMO-HN007	152	6	85.7	313	9	D80302
C 80	227	2	B1297998	B1297998	UI-R-CV2-	153	6	85.7	313	13	CW511846
C 81	227	7	B230266	B230266	251788 BA	154	6	85.7	314	5	CD856816
C 82	228	1	A1254348	A1254348	qu5c05.x	155	6	85.7	314	8	CN223696
C 83	228	1	AA612429	AA612429	vo5h04.x	156	6	85.7	316	8	CR740891
C 84	229	1	AV323627	AV323627	AV323627	157	6	85.7	318	7	BB252401
C 85	231	7	BB478527	BB478527	BB478527	158	6	85.7	318	11	BB491696
C 86	232	8	CR519429	CR519429	CR519429	159	6	85.7	321	5	CD858065
C 87	236	4	EX838501	EX838501	EX838501	160	6	85.7	321	10	R02114
C 88	236	7	AW815701	AW815701	QVO-ST021	161	6	85.7	322	2	BG228330
C 89	237	1	A1280359	A1280359	Q194C11.x	162	6	85.7	322	13	CL706266
C 90	238	1	AA014107	AA014107	mh39f07.x	163	6	85.7	324	2	BG210367
C 91	238	1	A1370845	A1370845	ta63f12.x	164	6	85.7	324	10	DY244238
C 92	241	5	CK261554	CK261554	ESW707632	165	6	85.7	335	13	CW511508
C 93	244	2	BG588726	BG588726	ESW490535	166	6	85.7	337	1	AA118077
C 94	247	11	AZ464767	AZ464767	1M0274L16	167	6	85.7	337	13	CL631399
C 95	250	1	AV292176	AV292176	AV292176	168	6	85.7	339	3	BM934523
C 96	251	3	BQ007023	BQ007023	UI-H-E11-	169	6	85.7	339	5	CD857729
C 97	252	1	A1934697	A1934697	wp88b10.x	170	6	85.7	339	10	F11225
C 98	252	7	AW663956	AW663956	hi76b08.x	171	6	85.7	330	11	AZ462826
C 99	252	7	B9590873	B9590873	UI-M-BH4-	172	6	85.7	331	7	BB532596
C 100	253	9	D801176	D801176	HUM043D12A	173	6	85.7	333	7	AW125571
C 101	254	8	CR462247	CR462247	CR462247	174	6	85.7	333	7	BE955670
C 102	254	9	D80313	D80313	HUM061E12B	175	6	85.7	333	12	CG485974
C 103	255	2	BG374398	BG374398	UI-R-CV1-	176	6	85.7	335	14	CR294455
C 104	255	2	BG811010	BG811010	da38d06	177	6	85.7	336	2	BI028828
C 105	256	10	DW123126	DW123126	CLRZ5518	178	6	85.7	336	3	BO988183
C 106	257	7	BF447024	BF447024	7067C09.x	179	6	85.7	338	1	AI414371
C 107	258	10	DV414893	DV414893	NADW050TR	180	6	85.7	338	1	AO022166
C 108	262	2	B1297375	B1297375	UI-R-CV2-	181	6	85.7	338	11	AG704781
C 109	262	2	BI300146	BI300146	UI-R-CV2-	182	6	85.7	339	12	CG577791
C 110	263	7	BP439867	BP439867	nab71a10	183	6	85.7	340	1	AI237331
C 111	264	7	B214710	B214710	BB214710	184	6	85.7	340	7	AW814070
C 112	268	10	DV771843	DV771843	McClIntoc	185	6	85.7	340	9	CX562950
C 113	268	12	CE338107	CE338107	tigr-g88-	186	6	85.7	340	10	DY052161
C 114	270	12	CG487381	CG487381	OST22865	187	6	85.7	341	4	BY111013
C 115	271	4	CA428913	CA428913	UI-H-PH1-	188	6	85.7	342	2	BF886333
C 116	271	9	D80236	D80236	HUM048F09A	189	6	85.7	343	4	CB693519
C 117	271	9	BU069751	BU069751	im39d2.y	190	6	85.7	343	14	CR136338
C 118	279	1	AA679398	AA679398	z129a09.s	191	6	85.7	344	1	AA469244
C 119	279	2	BG759088	BG759088	602710724	192	6	85.7	344	4	BM916886
C 120	279	7	AW485727	AW485727	67446 MAR	193	6	85.7	345	7	BB314189
C 121	279	7	BB309106	BB309106	BB309106	194	6	85.7	347	1	AA998110
C 122	280	7	B3112871	B3112871	BB112871	195	6	85.7	347	12	CG487031
C 123	285	1	AA468535	AA468535	ne66903.s	196	6	85.7	349	7	BB314013
C 124	285	11	AQ387436	AQ387436	RFC111-13	197	6	85.7	350	1	AA030161
C 125	286	8	CO873481	CO873481	BoVGen_01	198	6	85.7	350	12	CG493272
C 126	286	8	CO876640	CO876640	BoVGen_04	199	6	85.7	352	10	N74614
C 127	288	2	BG204927	BG204927	RST24344	200	6	85.7	353	7	AW008907
C 128	288	3	BQ648917	BQ648917	QGA8H16.y	201	6	85.7	353	12	CE707150
C 129	288	4	EX303555	EX303555	EX303555	202	6	85.7	355	8	CK977658
C 130	289	1	AI711077	AI711077	UI-R-AE1-	203	6	85.7	356	7	AV775301
C 131	289	3	BW510733	BW510733	BW510733	204	6	85.7	357	9	DA719661
C 132	290	4	CD077602	CD077602	MA3-9999U	205	6	85.7	359	1	AA647386
C 133	290	5	CD705379	CD705379	EST21906	206	6	85.7	359	1	AA726908
C 134	290	11	B37454	B37454	HS-1043-B2-	207	6	85.7	362	12	CG564561
C 135	291	7	BF560952	BF560952	UI-R-E1-f	208	6	85.7	363	7	BO584567
C 136	294	1	AA291494	AA291494	zt41909.s	209	6	85.7	363	7	BB805097
C 137	294	10	DY152116	DY152116	000508BTTN	210	6	85.7	363	12	CE760902
C 138	295	1	AA907539	AA907539	om09b03.s	211	6	85.7	365	3	BU522899
C 139	295	1	AV141194	AV141194	AV141194	212	6	85.7	365	11	AZ482660
C 140	295	8	CR461685	CR461685	CR461685	213	6	85.7	366	12	CG483920
C 141	296	1	AV086855	AV086855	AV086855	214	6	85.7	366	13	CL610380
C 142	297	2	BG730052	BG730052	de09b09.y	215	6	85.7	367	2	BG088127
C 143	298	7	BB458994	BB458994	BB458994	216	6	85.7	367	14	CR148713
C 144	299	1	AA473686	AA473686	vg89c04.r	217	6	85.7	368	10	DY042483
C 145	301	11	AQ632796	AQ632796	RPCI-11-4	218	6	85.7	369	13	CL569078
C 146	305	8	CO886548	CO886548	BoVGen_14	219	6	85.7	370	3	BP386340
C 147	306	12	CG561977	CG561977	OST184001	220	6	85.7	370	12	CG513120
C 148	308	1	AU150143	AU150143	AU150143	221	6	85.7	371	2	BU959532
C 149	308	7	BB280190	BB280190	BB280190	222	6	85.7	372	1	AA642191
C 150	310	10	DW164699	DW164699	CLVY3240	223	6	85.7	372	1	AI216186

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 12, 2006, 21:37:51 ; Search time 852 Seconds
(without alignments)
151.432 Million cell updates/sec

Title: US-10-537-648-1
Perfect score: 7
Sequence: 1 YLTPQS 7

Scoring table:

OLIGO	
Xgapop 60.0 , Xgapext 60.0	
Ygapop 60.0 , Ygapext 60.0	
Fgapop 60.0 , Fgapext 7.0	
Delop 60.0 , Delext 60.0	

Searched: 18892170 seqs, 6143817638 residues

Word size: 1

Total number of hits satisfying chosen parameters: 37649232

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters: -DEV=xlh
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-Q=/abse/ABSSWEB_spool/US10537648/runat_12102006_151504_15561/app_query.fasta_1
-DB=Published Applications NA Main -OFMT=fastap -SUFFIX=p2n.olig.rnpbm
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-TRANS=human40.cdi -LIST=1000 -DLOCALIGN=200 -THR SCORE=quality -THR MIN=1
-ALIGN=100 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
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-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

Database : Published Applications NA Main:*

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
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- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
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- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq.*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C	2	6	85.7	22	11	US-10-310-914A-1212172 Sequence 1212172,
C	3	6	85.7	24	11	US-10-310-914A-581792 Sequence 581792,
	4	6	85.7	25	9	US-10-719-900-702816 Sequence 702816,
	5	6	85.7	25	11	US-10-932-182A-181503 Sequence 181503,
	6	6	85.7	180	9	US-10-67A-124A-4967 Sequence 4967, Ap
	7	6	85.7	201	9	US-10-719-993-4501 Sequence 4501, Ap
C	8	6	85.7	201	9	US-10-719-993-4507 Sequence 4507, Ap
C	9	6	85.7	201	9	US-10-719-993-4528 Sequence 4528, Ap
C	10	6	85.7	201	9	US-10-719-993-4534 Sequence 4534, Ap
C	11	6	85.7	201	9	US-10-719-993-4557 Sequence 4557, Ap
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C	15	6	85.7	201	9	US-10-719-993-4614 Sequence 4614, Ap
C	16	6	85.7	201	9	US-10-719-993-4620 Sequence 4620, Ap
	17	6	85.7	201	9	US-10-741-600-26779 Sequence 26779, A
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C	29	6	85.7	201	16	US-11-124-367A-2615 Sequence 2615, Ap
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C	31	6	85.7	201	16	US-11-124-367A-2632 Sequence 2632, Ap
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77	6	85.7	541	3	US-10-930-213-97	Sequence 97, Appl	c 150	6	85.7	635	12	US-10-301-480-182422	Sequence 182422,
78	6	85.7	543	4	US-09-925-065A-793236	Sequence 793236,	c 151	6	85.7	635	12	US-10-301-480-795831	Sequence 795831,
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84	6	85.7	547	12	US-10-301-480-1019035	Sequence 1019035,	c 157	6	85.7	639	7	US-10-027-632-26965	Sequence 26965, A
85	6	85.7	547	12	US-10-301-480-1078069	Sequence 1078069,	158	6	85.7	640	6	US-10-027-632-284217	Sequence 284217,
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96	6	85.7	555	12	US-10-301-480-816373	Sequence 816373,	c 169	6	85.7	657	5	US-09-925-065A-41772	Sequence 41772, A
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122	6	85.7	595	4	US-09-925-065A-588388	Sequence 588388,	c 195	6	85.7	771	5	US-09-925-065A-6799	Sequence 6799, Ap
123	6	85.7	595	4	US-09-925-065A-588388	Sequence 588388,	c 196	6	85.7	771	12	US-10-301-480-108036	Sequence 108036,
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142	6	85.7	632	4	US-09-925-065A-926348	Sequence 926348,	c 215	6	85.7	887	12	US-10-301-480-552401	Sequence 552401,
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 12, 2006, 21:08:51 ; Search time 145 Seconds

(without alignments)

135.494 Million cell updates/sec

Title: US-10-537-648-1

Perfect score: 7

Sequence: 1 YLTQPS 7

Scoring table:

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 Ygapop 60.0 , Ygapext 60.0
 Fgapop 60.0 , Fgapext 7.0
 Delop 60.0 , Delext 60.0

Searched: 1403666 seqs, 935554401 residues

Word size: 1

Total number of hits satisfying chosen parameters: 2786218

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:

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Database :

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Pred. No. is the number of results predicted by chance to have a
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 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	6	85.7	447	3	US-09-470-276-69
C 3	6	85.7	497	3	US-09-621-976-19020
C 4	6	85.7	601	3	US-09-949-016-30525
C 5	6	85.7	601	3	US-09-949-016-37144
C 6	6	85.7	601	3	US-09-949-016-37158
C 7	6	85.7	601	3	US-09-949-016-44638

8	6	85.7	601	3	US-09-949-016-76098	Sequence 76098, A
9	6	85.7	601	3	US-09-949-016-103077	Sequence 103077, A
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C 13	6	85.7	601	3	US-09-949-016-115734	Sequence 115734, A
C 14	6	85.7	601	3	US-09-949-016-115827	Sequence 115827, A
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C 16	6	85.7	601	3	US-09-949-016-116013	Sequence 116013, A
C 17	6	85.7	601	3	US-09-949-016-116106	Sequence 116106, A
C 18	6	85.7	601	3	US-09-949-016-116199	Sequence 116199, A
C 19	6	85.7	601	3	US-09-949-016-116292	Sequence 116292, A
C 20	6	85.7	601	3	US-09-949-016-116385	Sequence 116385, A
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C 22	6	85.7	601	3	US-09-949-016-146130	Sequence 146130, A
C 23	6	85.7	601	3	US-09-949-016-146398	Sequence 146398, A
C 24	6	85.7	601	3	US-09-949-016-148718	Sequence 148718, A
C 25	6	85.7	601	3	US-09-949-016-148719	Sequence 148719, A
C 26	6	85.7	601	3	US-09-949-016-165817	Sequence 165817, A
C 27	6	85.7	601	3	US-09-949-016-165818	Sequence 165818, A
C 28	6	85.7	601	3	US-09-949-016-184545	Sequence 184545, A
C 29	6	85.7	601	3	US-09-949-016-184546	Sequence 184546, A
C 30	6	85.7	601	3	US-09-949-016-186632	Sequence 186632, A
C 31	6	85.7	601	3	US-09-949-016-187964	Sequence 187964, A
C 32	6	85.7	672	4	US-09-605-703B-2663	Sequence 2663, Ap
C 33	6	85.7	892	3	US-09-533-559-532	Sequence 532, App
C 34	6	85.7	1116	3	US-09-543-681A-739	Sequence 739, App
C 35	6	85.7	1128	3	US-09-543-681A-41	Sequence 41, Appl
C 36	6	85.7	1216	3	US-08-838-151A-62	Sequence 62, Appl
C 37	6	85.7	2812	3	US-09-620-312D-624	Sequence 624, Appl
C 38	6	85.7	3999	2	US-08-971-244-1	Sequence 1, Appl
C 39	6	85.7	3999	3	US-09-286-891-1	Sequence 1, Appl
C 40	6	85.7	5345	3	US-08-044-618-7	Sequence 7, Appl
C 41	6	85.7	19152	3	US-09-949-016-121110	Sequence 12110, A
C 42	6	85.7	19153	3	US-09-949-016-15795	Sequence 15795, A
C 43	6	85.7	19826	3	US-09-949-016-16973	Sequence 16973, A
C 44	6	85.7	20598	3	US-09-533-995-10	Sequence 10, Appl
C 45	6	85.7	20598	3	US-10-139-667-10	Sequence 20, Appl
C 46	6	85.7	27150	3	US-09-593-828-20	Sequence 20, Appl
C 47	6	85.7	28198	3	US-09-949-016-12349	Sequence 12349, A
C 48	6	85.7	28198	3	US-09-949-016-16887	Sequence 16887, A
C 49	6	85.7	30656	3	US-09-949-016-14613	Sequence 14613, A
C 50	6	85.7	42376	3	US-09-949-016-16216	Sequence 16216, A
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C 55	6	85.7	44821	3	US-09-949-016-13764	Sequence 13764, A
C 56	6	85.7	51273	3	US-09-949-016-13018	Sequence 13018, A
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C 58	6	85.7	52530	3	US-09-949-016-13948	Sequence 13948, A
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C 62	6	85.7	94077	3	US-09-949-016-13635	Sequence 13635, A
C 63	6	85.7	94750	3	US-09-596-002-38	Sequence 38, Appl
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C 66	6	85.7	99916	3	US-09-816-095-3	Sequence 3, Appl
C 67	6	85.7	100863	3	US-09-949-016-17031	Sequence 17031, A
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C 80	6	85.7	126176	3	US-09-949-016-16138	Sequence 16138, A

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87	6	85.7	205044	3	US-09-949-016-15852	Sequence 15852, A	c 160	5	71.4	217	3	US-09-789-529-28	Sequence 28, Appl
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91	6	85.7	223471	3	US-09-949-016-12724	Sequence 12724, A	c 164	5	71.4	240	3	US-08-559-397A-9	Sequence 9, Appl
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104	5	71.4	25	2	US-08-859-998-44	Sequence 44, Appl	177	5	71.4	301	3	US-08-871-355A-22	Sequence 22, Appl
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112	5	71.4	27	3	US-08-920-919A-41	Sequence 41, Appl	c 185	5	71.4	327	4	US-09-880-107-294	Sequence 294, App
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124	5	71.4	35	3	US-09-374-671A-37	Sequence 37, Appl	c 197	5	71.4	384	3	US-09-640-211A-1956	Sequence 1956, Ap
125	5	71.4	35	5	US-10-196-107A-37	Sequence 37, Appl	198	5	71.4	387	3	US-09-973-278-826	Sequence 826, App
126	5	71.4	36	3	US-09-892-074-10	Sequence 10, Appl	199	5	71.4	388	3	US-09-513-999C-1746	Sequence 1746, Ap
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134	5	71.4	56	3	US-10-014-012-204	Sequence 204, App	207	5	71.4	416	3	US-08-945-140-5	Sequence 5, Appl
135	5	71.4	66	3	US-09-625-188-44	Sequence 44, Appl	208	5	71.4	421	3	US-09-513-999C-27809	Sequence 27809, A
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144	5	71.4	79	3	US-09-604-287A-304	Sequence 304, App	c 217	5	71.4	453	3	US-09-880-107-3518	Sequence 3518, Ap
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146	5	71.4	79	3	US-09-590-751A-304	Sequence 304, App	c 219	5	71.4	462	3	US-09-880-107-2495	Sequence 2495, Ap
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152	5	71.4	121	3	US-09-818-875-514	Sequence 514, App	c 225	5	71.4	485	3	US-09-621-976-15354	Sequence 15354, A
153	5	71.4	121	3	US-09-818-875-514	Sequence 514, App	c 226	5	71.4	485	3	US-09-621-976-15354	Sequence 15354, A

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SUMMARIES

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6	85.7	162	8	ACA01262	C. glutam
6	85.7	202	2	AH85742	Human sin
6	85.7	285	3	AACT75508	Human ORP
6	85.7	285	6	ABN17552	Human ORP
6	85.7	289	10	ABX83523	Corn ear-
6	85.7	294	6	ABL79862	Human ova
6	85.7	299	12	ADO41272	Human cDN
6	85.7	308	4	AAH10981	Human cDN
6	85.7	340	13	ADV40722	Rat cardi
6	85.7	347	10	ADB56138	Toxicity-
6	85.7	347	10	ADB56138	Primary r
6	85.7	376	6	ABN19259	Human ORP
6	85.7	392	5	AAH81562	Human dif
6	85.7	411	13	ACF86753	Human SIR
6	85.7	447	2	AAH05178	Human MSH
6	85.7	448	12	ADJ75991	Marker ge
6	85.7	461	13	ADU12670	Solid tum
6	85.7	469	6	ABSO7083	Human gen
6	85.7	492	13	ACF81501	Human SIR
6	85.7	517	4	AAH09146	Human cDN
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6	85.7	574	4	ABA61762	Human foe
6	85.7	574	4	AAI41679	Probe #10
6	85.7	574	4	AAK35966	Human bon
6	85.7	574	4	AAK10071	Human bra
6	85.7	574	4	ABS35668	Human liv
6	85.7	574	6	ABS10166	Human gen
6	85.7	576	12	ADO34573	Human SLI
6	85.7	584	10	ADK52858	Plant DNA
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6	85.7	672	14	AED72487	Corynebac
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6	85.7	749	3	AAO1846	Human col
6	85.7	762	13	ADT41963	Bacterial
6	85.7	830	11	ACL29407	Rice abio
6	85.7	852	10	ABX78336	Soybean s
6	85.7	852	15	AEF94154	Stress re
6	85.7	866	4	AAH34154	Human col
6	85.7	870	3	AAAC59004	Human sec
6	85.7	892	3	AAF08009	Fusarium
6	85.7	892	13	ADU52050	Fusarium
6	85.7	892	14	ADZ50053	Fusarium
6	85.7	993	8	ACA53447	Prokaryot
6	85.7	1041	10	ABX78337	Soybean s
6	85.7	1041	15	AEF94156	Stress re
6	85.7	1084	14	ABE11565	Hamster c
6	85.7	1116	8	ADA70953	Rice gene
6	85.7	1116	10	ADF00454	Bacterial
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6	85.7	1605	14	AED73304	Human dif
6	85.7	1734	15	AED73304	Human pla
6	85.7	1797	8	ACA54446	Prokaryot
6	85.7	1898	4	AAH17977	Human cDN
6	85.7	1932	10	ADE59433	Human gen
6	85.7	1943	5	AAAS45223	cDNA enco
6	85.7	2000	6	ABZ16565	Arabidops
6	85.7	2000	8	ADA68927	Arabidops
6	85.7	2000	9	ADA02929	Mouse Pik
6	85.7	2175	10	ADB72667	Mouse Pik
6	85.7	2175	10	ADC85409	Mouse Pik
6	85.7	2175	12	ADM74524	Murine ca

77	6	85.7	2178	9	ADB08415	AdB08415 Alloiococ	150	6	85.7	16555	4	AAK70102	AAK70102 Human imm
78	6	85.7	2178	9	ADB08417	AdB08417 Alloiococ	151	6	85.7	19969	4	AAK65309	AAK65309 Human imm
79	6	85.7	2178	9	ADB08413	AdB08413 Alloiococ	152	6	85.7	20598	4	AAK65309	AAK65309 Human imm
80	6	85.7	2209	4	AAH17074	AAH17074 Human CDN	153	6	85.7	20598	4	AAK65309	AAK65309 Human imm
81	6	85.7	2209	13	ADO87393	ADO87393 Human tum	154	6	85.7	20598	9	ACH00110	ACH00110 Human zal
82	6	85.7	2215	4	AAH15419	AAH15419 Human CDN	155	6	85.7	23885	4	AAK73173	AAK73173 Human imm
83	6	85.7	2232	6	ABK35916	ABK35916 CDNA sequ	156	6	85.7	23885	4	AAK70103	AAK70103 Human imm
84	6	85.7	2383	4	AAI93833	AAI93833 Human pol	157	6	85.7	24993	4	AAK65726	AAK65726 Human imm
85	6	85.7	2566	4	AAH17667	AAH17667 Human CDN	158	6	85.7	25373	12	ADK16022	ADK16022 Human mam
86	6	85.7	2569	10	ADC30261	ADC30261 Human nov	159	6	85.7	27150	4	AAK65726	AAK65726 Human imm
87	6	85.7	2607	12	ADQ67217	ADQ67217 Novel hum	160	6	85.7	27976	4	AAK70187	AAK70187 Human gly
88	6	85.7	2659	9	ABT43745	ABT43745 Molecule	161	6	85.7	27976	4	AAK70187	AAK70187 Human imm
89	6	85.7	2812	4	AAI58734	AAI58734 Human pol	162	6	85.7	32185	11	ACN44604	ACN44604 Mouse gen
90	6	85.7	2812	4	AAI60520	AAI60520 Human pol	163	6	85.7	32185	5	AAK30115	AAK30115 Human lun
91	6	85.7	2812	5	ADQ98954	ADQ98954 DNA encod	164	6	85.7	32189	10	ADB33452	ADB33452 Human nov
92	6	85.7	2812	9	ADB48714	ADB48714 Novel hum	165	6	85.7	32221	5	AAK30113	AAK30113 Human lun
93	6	85.7	2819	6	ABA93732	ABA93732 Human dif	166	6	85.7	32221	10	ADB33450	ADB33450 Human nov
94	6	85.7	2830	6	ABL58960	ABL58960 Human tum	167	6	85.7	37091	4	ABL14244	ABL14244 Drosophil
95	6	85.7	2830	12	ADL26751	ADL26751 Human SE2	168	6	85.7	39325	4	AAK81660	AAK81660 Human imm
96	6	85.7	2867	6	ABN84190	ABN84190 Human cel	169	6	85.7	39776	10	AAK51353	AAK51353 Human sec
97	6	85.7	2867	14	ADM14872	ADM14872 Human cel	170	6	85.7	41159	4	AAK65631	AAK65631 Human imm
98	6	85.7	2902	3	AAK46853	AAK46853 Arabidops	171	6	85.7	43950	6	AAK65631	AAK65631 Human imm
99	6	85.7	3256	5	ADL45276	ADL45276 Human ova	172	6	85.7	44617	12	ADQ97951	ADQ97951 Mouse can
100	6	85.7	3289	8	ABX34745	ABX34745 Human mdd	173	6	85.7	44728	13	ABD32556	ABD32556 Mouse can
101	6	85.7	3324	6	AAK594913	AAK594913 Human DNA	174	6	85.7	51157	13	ABD32986	ABD32986 Mouse can
102	6	85.7	3339	13	ACN38144	ACN38144 Tumour-as	175	6	85.7	52746	14	AEA61129	AEA61129 Human FLJ
103	6	85.7	3452	12	ADM79346	ADM79346 Mouse lym	176	6	85.7	54732	13	ABD33335	ABD33335 Human can
104	6	85.7	3454	6	AAH41009	AAH41009 Mouse Fl3	177	6	85.7	58922	13	ABD33407	ABD33407 Human can
105	6	85.7	3454	6	ABK72319	ABK72319 DNA encod	178	6	85.7	62658	13	ABD33339	ABD33339 Human can
106	6	85.7	3454	6	ABK72292	ABK72292 Lymphona	179	6	85.7	63115	10	ADC85419	ADC85419 Mouse Tle
107	6	85.7	3454	6	ABK72292	ABK72292 Lymphona	180	6	85.7	63294	9	ADA02939	ADA02939 Mouse Tle
108	6	85.7	3454	6	ABK72292	ABK72292 Lymphona	181	6	85.7	63294	12	ADM74534	ADM74534 Murine ca
109	6	85.7	3454	9	ABK72292	ABK72292 Lymphona	182	6	85.7	63294	12	ADM74534	ADM74534 Murine ca
110	6	85.7	3454	10	ADB72666	ADB72666 Mouse Pik	183	6	85.7	63294	11	ACN44106	ACN44106 Human gen
111	6	85.7	3454	10	ADB72666	ADB72666 Mouse Pik	184	6	85.7	63294	11	ACN44106	ACN44106 Human gen
112	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	185	6	85.7	80105	13	ABD33213	ABD33213 Murine ca
113	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	186	6	85.7	86431	6	ABQ74964	ABQ74964 7
114	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	187	6	85.7	86431	6	ABQ74964	ABQ74964 7
115	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	188	6	85.7	86765	14	AEH17778	AEH17778 Fibrotic
116	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	189	6	85.7	86765	14	AEH17778	AEH17778 Fibrotic
117	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	190	6	85.7	86765	14	AEH17778	AEH17778 Fibrotic
118	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	191	6	85.7	86765	14	AEH17778	AEH17778 Fibrotic
119	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	192	6	85.7	86765	14	AEH17778	AEH17778 Fibrotic
120	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	193	6	85.7	86765	14	AEH17778	AEH17778 Fibrotic
121	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	194	6	85.7	86765	14	AEH17778	AEH17778 Fibrotic
122	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	195	6	85.7	86765	14	AEH17778	AEH17778 Fibrotic
123	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	196	6	85.7	86765	14	AEH17778	AEH17778 Fibrotic
124	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	197	6	85.7	86765	14	AEH17778	AEH17778 Fibrotic
125	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	198	6	85.7	86765	14	AEH17778	AEH17778 Fibrotic
126	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	199	6	85.7	86765	14	AEH17778	AEH17778 Fibrotic
127	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	200	6	85.7	86765	14	AEH17778	AEH17778 Fibrotic
128	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	201	6	85.7	86765	14	AEH17778	AEH17778 Fibrotic
129	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	202	6	85.7	86765	14	AEH17778	AEH17778 Fibrotic
130	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	203	6	85.7	86765	14	AEH17778	AEH17778 Fibrotic
131	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	204	6	85.7	86765	14	AEH17778	AEH17778 Fibrotic
132	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	205	6	85.7	86765	14	AEH17778	AEH17778 Fibrotic
133	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	206	6	85.7	86765	14	AEH17778	AEH17778 Fibrotic
134	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	207	6	85.7	86765	14	AEH17778	AEH17778 Fibrotic
135	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	208	6	85.7	86765	14	AEH17778	AEH17778 Fibrotic
136	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	209	6	85.7	86765	14	AEH17778	AEH17778 Fibrotic
137	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	210	6	85.7	86765	14	AEH17778	AEH17778 Fibrotic
138	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	211	6	85.7	86765	14	AEH17778	AEH17778 Fibrotic
139	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	212	6	85.7	86765	14	AEH17778	AEH17778 Fibrotic
140	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	213	6	85.7	86765	14	AEH17778	AEH17778 Fibrotic
141	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	214	6	85.7	86765	14	AEH17778	AEH17778 Fibrotic
142	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	215	6	85.7	86765	14	AEH17778	AEH17778 Fibrotic
143	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	216	6	85.7	86765	14	AEH17778	AEH17778 Fibrotic
144	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	217	6	85.7	86765	14	AEH17778	AEH17778 Fibrotic
145	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	218	6	85.7	86765	14	AEH17778	AEH17778 Fibrotic
146	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	219	6	85.7	86765	14	AEH17778	AEH17778 Fibrotic
147	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	220	6	85.7	86765	14	AEH17778	AEH17778 Fibrotic
148	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	221	6	85.7	86765	14	AEH17778	AEH17778 Fibrotic
149	6	85.7	3454	12	ADM79373	ADM79373 Mouse lym	222	6	85.7	86765	14	AEH17778	AEH17778 Fibrotic

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 12, 2006, 21:02:56 ; Search time 3418 Seconds

(without alignments)
196.445 Million cell updates/sec

Title: US-10-537-648-1

Perfect score: 7

Sequence: 1 YLTQPS 7

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 60.0 , Fgapext 7.0
Delop 60.0 , Delext 60.0

Searched: 6366136 seqs, 31973710525 residues

Word size: 1

Total number of hits satisfying chosen parameters: 12697109

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:
-MODEL=frame+ p2n model -DEV=xlh
-Q/abs/ABSWEB_spool/US10537648/runat_12102006_151451_15373/app_query.fasta_1
-DB=GenEmbl -OFT=fastap -SUFFIX=p2n.olig.rge -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNIT=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=1000 -DOALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=100 -MODE=LOCAL
-OUTFMT=pcp -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs02h
-USER=US10537648 @CGN 1 1 5548 @runat_12102006_151451_15373 -NCPU=6 -ICPU=3
-NO_WMAP -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

Database :

GenEmbl.*
1: gb_env.*
2: gb_pat.*
3: gb_ph.*
4: gb_pl.*
5: gb_pr.*
6: gb_ro.*
7: gb_sts.*
8: gb_sy.*
9: gb_un.*
10: gb_vi.*
11: gb_ov.*
12: gb_htg.*
13: gb_in.*
14: gb_om.*
15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	100.0	21	2	CQ828007 Sequence
2	7	100.0	2000	2	AX656858 Sequence
3	7	100.0	44681	13	AC092520

4	7	100.0	69037	6	AC003949
5	7	100.0	92797	5	AF038458
6	7	100.0	99489	12	AC084843
7	7	100.0	103836	6	AC125670
8	7	100.0	105538	4	OSJN00043
9	7	100.0	110000	4	AP008207_428
10	7	100.0	110000	4	AP008210_007
11	7	100.0	112833	12	AC153744
12	7	100.0	130225	12	AC177977
13	7	100.0	131761	12	AC164507
14	7	100.0	135924	14	AC163264
15	7	100.0	137877	12	AC167095
16	7	100.0	139969	12	AC170718
17	7	100.0	144819	12	AC173446
18	7	100.0	148743	11	BX324154
19	7	100.0	151772	6	AC109294
20	7	100.0	155624	5	AC027058
21	7	100.0	165228	5	CNS01DMS
22	7	100.0	166758	12	AC173466
23	7	100.0	167388	12	AC157445
24	7	100.0	170875	6	AC154429
25	7	100.0	172427	5	AC161282
26	7	100.0	172853	5	AC084361
27	7	100.0	173555	4	AP003277
28	7	100.0	179085	5	AC175825
29	7	100.0	184106	12	AC144662
30	7	100.0	188181	5	AC073879
31	7	100.0	192769	11	BX571945
32	7	100.0	196040	12	BX936414
33	7	100.0	198138	6	AC108443
34	7	100.0	198392	11	CR383678
35	7	100.0	198694	6	BX072557
36	7	100.0	203905	12	AC166470
37	7	100.0	205476	12	AC139733
38	7	100.0	211542	6	AC126275
39	7	100.0	212186	6	AC122337
40	7	100.0	213556	6	AC127294
41	7	100.0	215694	12	AC162334
42	7	100.0	216921	12	BX322658
43	7	100.0	218094	12	AC094408
44	7	100.0	219298	6	AC161378
45	7	100.0	227489	12	AC117015
46	7	100.0	229617	12	AC110849
47	7	100.0	231580	12	AC136817
48	7	100.0	232346	6	CR974489
49	7	100.0	235024	12	AC120681
50	7	100.0	235183	12	AC079427
51	7	100.0	236235	12	AC120331
52	7	100.0	239915	6	AC124977
53	7	100.0	241481	12	AC098105
54	7	100.0	241481	12	AC160175
55	7	100.0	246996	12	AC096933
56	7	100.0	259204	12	AC095370
57	7	100.0	271699	12	AC095812
58	7	100.0	282933	12	AC122970
59	7	100.0	295904	12	AC119509
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61	6	85.7	170	7	G20553
62	6	85.7	180	7	AB143874
63	6	85.7	202	7	G54653
64	6	85.7	202	7	G60148
65	6	85.7	227	7	HUMSTAF
66	6	85.7	240	2	CQ820279
67	6	85.7	240	10	AV303046
68	6	85.7	250	5	AJ628945
69	6	85.7	285	2	CQ437821
70	6	85.7	289	2	AR246624
71	6	85.7	294	2	CQ460062
72	6	85.7	296	15	AF536468
73	6	85.7	298	15	AF536466
74	6	85.7	308	2	BD152973
75	6	85.7	308	2	AX872911
76	6	85.7	321	10	AF113567

AC003949	Mus muscu
AF038458	Homo sapi
AC084843	Homo sapi
AC125670	Rattus no
AL066612	Oryza sat
Continuation (429	
Continuation (8 of	
AC153744	Ornithorh
AC177977	Strongylo
AC164507	Loxodont
AC163264	Rhinoloph
AC167095	Sorex ara
AC170718	Ateles
AC173446	Ateles
BX324154	Zebrafish
AC109294	Mus muscu
AC027058	Homo sapi
AL138479	Human chr
AC173466	Sorex ara
AC157445	Sus scro
AC154429	Mus muscu
AC161282	Pan trogl
AC084361	Homo sapi
AP003277	Oryza sat
AC175825	Pan trogl
AC144662	Rattus no
AC073879	Homo sapi
BX571945	Zebrafish
BX936414	Danio rer
AC108443	Mus muscu
CR383678	Zebrafish
BX072557	Mouse DNA
AC166470	Bos tauru
AC139733	Sus scro
AC126275	Mus muscu
AC122337	Mus muscu
AC127294	Mus muscu
AC162334	Bos tauru
BX322658	Mus muscu
AC094408	Rattus no
AC161378	Mus muscu
AC117015	Rattus no
AC110849	Rattus no
AC136817	Rattus no
CR974489	Mouse DNA
AC120681	Rattus no
AC079427	Mus muscu
AC120331	Rattus no
AC124977	Mus muscu
AC098105	Rattus no
AC160175	Bos tauru
AC096933	Rattus no
AC095370	Rattus no
AC095812	Rattus no
AC122970	Rattus no
AC119509	Rattus no
CQ654264	Sequence
G20553	human STS A
AB143874	Homo sapi
G54653	AffySTS0000
G60148	SHGC-130789
M83622	Human satel
CQ820279	Sequence
AV303046	Untyped h
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CQ437821	Sequence
AR246624	Sequence
CQ460062	Sequence
AF536468	Nocardia
AF536466	Nocardia
BD152973	Primer fo
AX872911	Sequence
AF113567	HIV-1 iso

C 77	6	85.7	326	5	HSRPS26D	X79236 Homo sapien	150	6	85.7	903	10	AB055923
C 78	6	85.7	334	7	BV244336	BV244336 S234P626F	151	6	85.7	903	10	AB055924
C 79	6	85.7	376	2	CQ441235	CQ441235 Sequence	152	6	85.7	927	15	AF261151
C 80	6	85.7	391	7	G50827	G50827 SHGC-81169	153	6	85.7	1021	2	CQ731389
C 81	6	85.7	391	11	PCMSAT6FR	Y12771 Phalacrocor	154	6	85.7	1038	4	AF490530
C 82	6	85.7	392	2	AX210429	AX210429 Sequence	155	6	85.7	1084	2	CS211757
C 83	6	85.7	447	2	AR443227	AR443227 Sequence	156	6	85.7	1084	6	CGUI2420
C 84	6	85.7	448	2	CQ777557	CQ777557 Sequence	157	6	85.7	1086	6	AY157969
C 85	6	85.7	448	7	HSC11106	AL158267 H.sapiens	158	6	85.7	1116	2	AR375733
C 86	6	85.7	461	2	CQ921909	CQ921909 Sequence	159	6	85.7	1116	2	AX654406
C 87	6	85.7	469	2	CQ295969	CQ295969 Sequence	160	6	85.7	1128	2	AR375035
C 88	6	85.7	477	13	AY598732	AY598732 Eulalia v	161	6	85.7	1142	11	CR390914
C 89	6	85.7	480	7	G34628	G34628 human SFS	162	6	85.7	1198	11	BX950293
C 90	6	85.7	491	7	G99807	G99807 S208P601PC	163	6	85.7	1216	2	AR170810
C 91	6	85.7	497	2	AX988217	AX988217 Sequence	164	6	85.7	1250	13	TFU85621
C 92	6	85.7	497	2	BD123076	BD123076 EST and e	165	6	85.7	1285	6	MYORF
C 93	6	85.7	497	2	AR427523	AR427523 Sequence	166	6	85.7	1321	13	AY617385
C 94	6	85.7	511	7	BV292235	BV292235 S232P6459	167	6	85.7	1378	14	AY377346
C 95	6	85.7	517	2	BD151138	BD151138 Primer fo	168	6	85.7	1380	13	AF100647
C 96	6	85.7	517	2	CQ717985	CQ717985 Sequence	169	6	85.7	1436	2	AX025512
C 97	6	85.7	517	2	AX871076	AX871076 Sequence	170	6	85.7	1436	5	HSU63108
C 98	6	85.7	541	2	AX210455	AX210455 Sequence	171	6	85.7	1452	4	RICMTB2
C 99	6	85.7	553	7	G90457	G90457 S208P6416RE	172	6	85.7	1485	2	AX463562
C 100	6	85.7	566	7	BV103893	BV103893 MARC 4607	173	6	85.7	1539	2	AX463562
C 101	6	85.7	574	2	CQ101506	CQ101506 Sequence	174	6	85.7	1546	4	MIOSELB2
C 102	6	85.7	574	2	CQ140501	CQ140501 Sequence	175	6	85.7	1591	2	BD160574
C 103	6	85.7	574	2	CQ223819	CQ223819 Sequence	176	6	85.7	1591	2	AX883862
C 104	6	85.7	574	2	CQ261806	CQ261806 Sequence	177	6	85.7	1591	5	AK024303
C 105	6	85.7	574	2	CQ299052	CQ299052 Sequence	178	6	85.7	1605	2	E64409
C 106	6	85.7	574	2	CQ335968	CQ335968 Sequence	179	6	85.7	1605	2	AX210627
C 107	6	85.7	580	6	MMU50414	U50414 Mus musculus	180	6	85.7	1605	5	AB015345
C 108	6	85.7	589	7	BV356736	BV356736 S231P668R	181	6	85.7	1647	4	DQ056727
C 109	6	85.7	596	6	AB038243	AB038243 Mus muscu	182	6	85.7	1683	5	BC043226
C 110	6	85.7	613	7	BV068685	BV068685 S212P6320	183	6	85.7	1694	4	BC032406
C 111	6	85.7	632	7	BV356359	BV356359 S231P6201	184	6	85.7	1743	4	AK067423
C 112	6	85.7	660	2	BD162314	BD162314 Novel pol	185	6	85.7	1748	6	BC079216
C 113	6	85.7	660	2	AX120197	AX120197 Sequence	186	6	85.7	1755	5	BC026075
C 114	6	85.7	669	7	BV078027	BV078027 S212P6035	187	6	85.7	1755	13	AY060295
C 115	6	85.7	672	2	AR764881	AR764881 Sequence	188	6	85.7	1802	5	BC024183
C 116	6	85.7	681	2	BD149055	BD149055 Primer fo	189	6	85.7	1802	5	BC034491
C 117	6	85.7	681	2	AX868993	AX868993 Sequence	190	6	85.7	1829	13	EZ08TUB
C 118	6	85.7	691	14	DQ218446	DQ218446 Sus scrof	191	6	85.7	1834	6	AB016768
C 119	6	85.7	693	7	BV252516	BV252516 S234P6375	192	6	85.7	1848	14	BC111324
C 120	6	85.7	710	7	BV501024	BV501024 S222P6206	193	6	85.7	1886	6	BC027256
C 121	6	85.7	724	10	AB167995	AB167995 Human ech	194	6	85.7	1886	2	BD159969
C 122	6	85.7	726	11	CAM290505	AJ290505 Callia am	195	6	85.7	1898	5	AX882860
C 123	6	85.7	730	11	BX930880	BX930880 Gallus ga	196	6	85.7	1898	5	AK023362
C 124	6	85.7	731	11	BX933282	BX933282 Gallus ga	197	6	85.7	1913	5	AX025782
C 125	6	85.7	746	11	BX933329	BX933329 Gallus ga	198	6	85.7	1931	5	AK027291
C 126	6	85.7	749	2	BD220724	BD220724 Human gen	199	6	85.7	1960	5	HSMH3
C 127	6	85.7	751	5	BSA324854	AJ324854 Homo sapi	200	6	85.7	1981	5	AK056166
C 128	6	85.7	775	7	BA484934	BA484934 S217P6147	201	6	85.7	2000	2	AX509675
C 129	6	85.7	782	7	BA496165	BA496165 S217P6147	202	6	85.7	2000	2	AX523380
C 130	6	85.7	788	7	BV633139	BV633139 S216P6218	203	6	85.7	2014	11	BC076289
C 131	6	85.7	790	4	AY183020	AY183020 Trifolium	204	6	85.7	2119	6	BC051106
C 132	6	85.7	802	7	BV656636	BV656636 S217P6192	205	6	85.7	2175	2	DD164600
C 133	6	85.7	804	5	HSMH3V6	AF070077 Homo sapi	206	6	85.7	2175	2	AX695820
C 134	6	85.7	814	7	BV649478	BV649478 S216P6142	207	6	85.7	2199	13	AF003342
C 135	6	85.7	835	4	AF162210	AF162210 Lactuca s	208	6	85.7	2209	2	BD159066
C 136	6	85.7	836	7	BV612195	BV612195 S217P6150	209	6	85.7	2209	2	AX881484
C 137	6	85.7	837	7	BV618122	BV618122 S217P6186	210	6	85.7	2209	5	AK021622
C 138	6	85.7	846	6	BC054440	BC054440 Mus muscu	211	6	85.7	2215	2	BD157411
C 139	6	85.7	857	7	BA4833129	BA4833129 S1X4f03	212	6	85.7	2215	2	AX878726
C 140	6	85.7	864	7	CNS06K5L	AL402463 17 end of	213	6	85.7	2229	7	BV178520
C 141	6	85.7	870	2	BD249974	BD249974 50 human	214	6	85.7	2252	5	HSU41448
C 142	6	85.7	870	7	BV520464	BV520464 G591P6455	215	6	85.7	2276	4	CAR250836
C 143	6	85.7	880	6	BC013618	BC013618 Mus muscu	216	6	85.7	2353	5	BC035166
C 144	6	85.7	883	11	AY626691	AY626691 Saprosin	217	6	85.7	2418	5	AB063085
C 145	6	85.7	883	11	AY626692	AY626692 Saprosin	218	6	85.7	2422	5	BC063873
C 146	6	85.7	884	7	BA467774	BA467774 G591P6001	219	6	85.7	2496	5	AK092325
C 147	6	85.7	888	11	BX930800	BX930800 Gallus ga	220	6	85.7	2514	6	RNU84612
C 148	6	85.7	888	11	BX930832	BX930832 Gallus ga	221	6	85.7	2541	11	AY735397
C 149	6	85.7	892	2	AR671031	AR671031 Sequence	222	6	85.7	2566	2	BD159659

AB055923	Human ech
AB055924	Human ech
AF261151	Vibrio ch
CQ731389	Sequence
AF490530	Lycopersi
CS211757	Sequence
UI2420	Cricetus
AY157969	Rattus no
AR375733	Sequence
AX654406	Sequence
AR375035	Sequence
CR390914	Gallus ga
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AR170810	Sequence
U85621	Trichomo
X05260	Mouse Y chr
AY617385	Sterkiell
AY377346	Gulo gulo
AF100647	Trypanoso
AX025512	Sequence
AX883862	Sequence
AK024303	Homo sapi
U63108	Human eukar
D00564	Oryza sativ
AX463562	Sequence
X16153	Rice mitoch
BD160574	Primer fo
AX883862	Sequence
AK024303	Homo sapi
E64409	Peptide hav
AX210627	Sequence
AB015345	Homo sapi
DQ056727	Arabidops
BC043226	Homo sapi
BC032406	Homo sapi
AK067423	Oryza sat
BC079216	Rattus no
BC026075	Homo sapi
AY060295	Drosophil
BC024183	Homo sapi
BC034491	Homo sapi
LA7271	Encephalito
AB016768	Mus muscu
BC111324	Bos tauru
BD27256	Mus muscu
BD159969	Primer fo
AX882860	Sequence
AK023362	Homo sapi
AK023362	Homo sapi
AB072791	Macaca fa
AF048990	Homo sapi
AX509675	Homo sapi
AX523380	Sequence
BC076289	Danio rer
BC051106	Mus muscu
DD164600	NOVEL COM
AX695820	Sequence
AF003342	Drosophil
BD159066	Primer fo
AX881484	Sequence
AK021622	Homo sapi
BD157411	Primer fo
AX878726	Sequence
AK021844	Homo sapi
U41448	Homo sapien
U41448	Homo sapien
AJ550836	Ciccar ari
BC035166	Homo sapi
AB063085	Macaca fa
BC063873	Homo sapi
AK092325	Homo sapi
U82612	Rattus norv
AY735397	Danio rer
BD159659	Primer fo

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 12, 2006, 20:46:38 ; Search time 164 Seconds
(without alignments)
119.628 Million cell updates/sec

Title: US-10-537-648-1

Perfect score: 37

Sequence: 1 YLTQPOS 7

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 2395520 seqs, 934235491 residues

Total number of hits satisfying chosen parameters: 4791040

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Command line parameters:

-MODEL=frame_p2n.model -DSV=xlh

-Q=/abss/ABSSWEB_spool/US10537648/runat_12102006_151437_15215/app_query.fasta.1

-DB=Published Applications NA New -QMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1

-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blsum62

-TRANS=human40.cdi -LIST=1000 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100

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-MINLEN=0 -MAXLEN=200000000 -HOST=abs03h

-USER=US10537648 @CGN_1_1_238 @runat_12102006_151437_15215 -NCPU=6 -ICPU=3

-NO WMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120

-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7

-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

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1	37	100.0	21	6	US-10-537-648-28
2	34	91.9	864	8	US-11-266-748A-369640
3	34	91.9	864	8	US-11-266-748A-453019
4	34	91.9	2000	7	US-11-299-286-4370
5	34	91.9	59637	6	US-10-539-228-311
6	34	91.9	124074	8	US-11-266-748A-28242
7	34	91.9	128963	6	US-10-540-898-86
					Sequence 28, Appl
					Sequence 369640,
					Sequence 453019,
					Sequence 4370, Ap
					Sequence 311, App
					Sequence 28242, A
					Sequence 86, Appl

Sequence 21, Appl
Sequence 181503,
Sequence 172570,
Sequence 229588,
Sequence 88725, A
Sequence 141536,
Sequence 84513, A
Sequence 111869,
Sequence 137324,
Sequence 40157, A
Sequence 40156, A
Sequence 197849,
Sequence 69213, A
Sequence 122024,
Sequence 173755,
Sequence 186472,
Sequence 193735,
Sequence 57572, A
Sequence 4625, Ap
Sequence 26861, A
Sequence 56273, A
Sequence 414, App
Sequence 526, App
Sequence 658, App
Sequence 69, Appl
Sequence 139, App
Sequence 15474, A
Sequence 28043, A
Sequence 9198, Ap
Sequence 6, Appl
Sequence 105136,
Sequence 116375,
Sequence 37813, A
Sequence 187888,
Sequence 242100,
Sequence 7, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 492, App
Sequence 29071, A
Sequence 28884, A
Sequence 32, Appl
Sequence 805, App
Sequence 848, App
Sequence 59424, A
Sequence 22658, A
Sequence 1232, Ap
Sequence 1, Appl
Sequence 372269,
Sequence 58280, A
Sequence 79854, A
Sequence 132665,
Sequence 8419, Ap
Sequence 201211,
Sequence 202914,
Sequence 204922,
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Sequence 131792,
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Sequence 4314, Ap
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C 81	31	83.8	2713	6	US-10-449-902-21193	Sequence 21193, A	C 154	30	81.1	1000	8	US-11-266-748A-196663	Sequence 196663,
C 82	31	83.8	2824	8	US-11-293-697-1307	Sequence 1307, Ap	C 155	30	81.1	1000	8	US-11-266-748A-199525	Sequence 199525,
C 83	31	83.8	3141	8	US-11-266-748A-23592	Sequence 23592, A	C 156	30	81.1	1000	8	US-11-266-748A-202243	Sequence 202243,
C 84	31	83.8	3472	9	US-11-218-305-22603	Sequence 22603, A	C 157	30	81.1	1000	8	US-11-266-748A-203661	Sequence 203661,
C 85	31	83.8	5087	6	US-10-517-441-594	Sequence 594, App	C 158	30	81.1	1000	8	US-11-266-748A-221613	Sequence 221613,
C 86	31	83.8	5087	6	US-10-517-441-654	Sequence 654, App	C 159	30	81.1	1000	8	US-11-266-748A-222435	Sequence 222435,
C 87	31	83.8	15225	6	US-10-934-003-2	Sequence 2, Appli	C 160	30	81.1	1000	8	US-11-266-748A-223483	Sequence 223483,
C 88	31	83.8	80988	6	US-10-669-920-261	Sequence 261, App	C 161	30	81.1	1000	8	US-11-266-748A-283012	Sequence 283012,
C 89	31	83.8	95963	9	US-11-021-837-39	Sequence 39, Appl	C 162	30	81.1	1000	8	US-11-266-748A-288654	Sequence 288654,
C 90	31	83.8	101954	6	US-10-539-228-782	Sequence 782, App	C 163	30	81.1	1000	8	US-11-266-748A-291113	Sequence 291113,
C 91	31	83.8	107543	6	US-10-539-228-706	Sequence 706, App	C 164	30	81.1	1000	8	US-11-266-748A-309652	Sequence 309652,
C 92	31	83.8	110799	6	US-10-540-898-790	Sequence 790, App	C 165	30	81.1	1000	8	US-11-266-748A-340083	Sequence 340083,
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C 94	31	83.8	215126	6	US-10-540-898-339	Sequence 339, App	C 167	30	81.1	1000	8	US-11-266-748A-392639	Sequence 392639,
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C 97	31	83.8	1320443	6	US-10-833-833-77	Sequence 77, Appl	C 170	30	81.1	1000	8	US-11-266-748A-402494	Sequence 402494,
C 98	30	81.1	48	7	US-11-434-137-11221	Sequence 11221, A	C 171	30	81.1	1000	8	US-11-266-748A-468268	Sequence 468268,
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C 103	30	81.1	306	8	US-11-266-748A-59976	Sequence 59976, A	C 176	30	81.1	1019	9	US-11-056-355B-57641	Sequence 57641, A
C 104	30	81.1	354	8	US-11-266-748A-62972	Sequence 62972, A	C 177	30	81.1	1024	8	US-11-266-748A-257846	Sequence 257846,
C 105	30	81.1	354	8	US-11-266-748A-65804	Sequence 65804, A	C 178	30	81.1	1024	8	US-11-266-748A-278254	Sequence 278254,
C 106	30	81.1	354	8	US-11-314-834-2038	Sequence 2038, App	C 179	30	81.1	1024	8	US-11-266-748A-318363	Sequence 318363,
C 107	30	81.1	385	7	US-11-314-834-2038	Sequence 2038, App	C 180	30	81.1	1026	8	US-11-266-748A-368643	Sequence 368643,
C 108	30	81.1	415	8	US-11-266-748A-37093	Sequence 37093, A	C 181	30	81.1	1026	8	US-11-266-748A-452022	Sequence 452022,
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C 113	30	81.1	469	8	US-11-266-748A-60751	Sequence 60751, A	C 186	30	81.1	1169	8	US-11-266-748A-112073	Sequence 112073,
C 114	30	81.1	486	8	US-11-266-748A-212034	Sequence 212034, A	C 187	30	81.1	1169	8	US-11-266-748A-138543	Sequence 138543,
C 115	30	81.1	486	8	US-11-266-748A-235549	Sequence 235549, A	C 188	30	81.1	1281	8	US-11-266-748A-362449	Sequence 362449,
C 116	30	81.1	500	8	US-11-266-748A-38188	Sequence 38188, A	C 189	30	81.1	1281	8	US-11-266-748A-445828	Sequence 445828,
C 117	30	81.1	505	8	US-11-266-748A-385441	Sequence 385441, A	C 190	30	81.1	1291	8	US-11-266-748A-20657	Sequence 20657, A
C 118	30	81.1	505	8	US-11-266-748A-448820	Sequence 448820, A	C 191	30	81.1	1345	8	US-11-216-545-1473	Sequence 1473, Ap
C 119	30	81.1	508	8	US-11-266-748A-269980	Sequence 269980, A	C 192	30	81.1	1368	6	US-10-449-902-18929	Sequence 18929, A
C 120	30	81.1	508	8	US-11-266-748A-330497	Sequence 330497, A	C 193	30	81.1	1441	8	US-11-266-748A-79600	Sequence 79600, A
C 121	30	81.1	522	6	US-10-834-268-4547	Sequence 4547, App	C 194	30	81.1	1441	8	US-11-266-748A-132411	Sequence 132411,
C 122	30	81.1	535	6	US-10-834-268-549	Sequence 549, App	C 195	30	81.1	1515	6	US-10-539-450-3	Sequence 3, Appli
C 123	30	81.1	544	8	US-11-266-748A-377797	Sequence 377797, A	C 196	30	81.1	1559	9	US-11-218-305-23692	Sequence 23692, A
C 124	30	81.1	544	8	US-11-266-748A-461176	Sequence 461176, A	C 197	30	81.1	1614	9	US-11-056-355B-78416	Sequence 78416, A
C 125	30	81.1	549	8	US-11-266-748A-55250	Sequence 55250, A	C 198	30	81.1	1661	6	US-10-449-902-8619	Sequence 8619, Ap
C 126	30	81.1	570	8	US-11-266-748A-182936	Sequence 182936, A	C 199	30	81.1	1696	6	US-10-449-902-27800	Sequence 27800, Ap
C 127	30	81.1	571	7	US-11-292-078-9594	Sequence 9594, App	C 200	30	81.1	1743	6	US-10-449-902-15954	Sequence 15954, A
C 128	30	81.1	584	8	US-11-266-748A-44818	Sequence 44818, A	C 201	30	81.1	1771	8	US-11-266-748A-258221	Sequence 258221,
C 129	30	81.1	600	8	US-11-266-748A-47673	Sequence 47673, A	C 202	30	81.1	1771	8	US-11-266-748A-318738	Sequence 318738,
C 130	30	81.1	669	8	US-11-266-748A-209838	Sequence 209838, A	C 203	30	81.1	1808	6	US-10-449-902-2462	Sequence 2462, Ap
C 131	30	81.1	669	8	US-11-266-748A-234204	Sequence 234204, A	C 204	30	81.1	1875	8	US-11-217-525-4544	Sequence 4544, Ap
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C 140	30	81.1	803	8	US-11-266-748A-85968	Sequence 85968, A	C 214	30	81.1	2157	8	US-11-293-697-2426	Sequence 2426, Ap
C 141	30	81.1	803	8	US-11-266-748A-138779	Sequence 138779, A	C 215	30	81.1	2181	8	US-11-266-748A-61640	Sequence 61640, Ap
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C 147	30	81.1	873	8	US-11-266-748A-191504	Sequence 191504, A	C 221	30	81.1	2406	8	US-11-056-355B-101199	Sequence 101199, A
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 12, 2006, 20:46:08 ; Search time 1456 Seconds
(without alignments)
88.613 Million cell updates/sec

Title: US-10-537-648-1

Perfect score: 37

Sequence: 1 YLTPQS 7

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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C 79	33	89.2	506	5	US-10-301-480-890550	Sequence 890550,	152	33	89.2	1216	2	US-08-838-151A-62	Sequence 62, Appl
C 80	33	89.2	506	5	US-09-925-065A-775527	Sequence 775527,	153	33	89.2	1216	2	US-10-932-182A-173755	Sequence 173755,
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C 83	33	89.2	506	5	US-09-925-065A-775530	Sequence 775530,	156	33	89.2	1216	2	US-10-292-798-257	Sequence 257, App
C 84	33	89.2	506	5	US-09-925-065A-775531	Sequence 775531,	157	33	89.2	1216	2	US-09-925-065A-703088	Sequence 703088,
C 85	33	89.2	506	5	US-09-925-065A-775532	Sequence 775532,	158	33	89.2	1216	2	US-09-925-065A-703088	Sequence 703088,
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C 87	33	89.2	506	5	US-09-925-065A-775534	Sequence 775534,	160	33	89.2	1216	2	US-09-925-065A-703088	Sequence 703088,
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C 92	33	89.2	506	5	US-09-925-065A-193775	Sequence 193775,	165	33	89.2	1216	2	US-10-501-282-2357	Sequence 2357, App
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C 102	33	89.2	506	5	US-09-925-065A-372550	Sequence 372550,	175	33	89.2	1216	2	US-10-719-993-322	Sequence 322, App
C 103	33	89.2	506	5	US-10-301-480-283164	Sequence 283164,	176	33	89.2	1216	2	US-11-124-367A-134	Sequence 134, App
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C 139	33	89.2	506	5	US-10-301-480-108036	Sequence 108036,	212	33	89.2	1216	2	US-10-209-787-513	Sequence 513, App
C 140	33	89.2	506	5	US-10-301-480-721445	Sequence 721445,	213	33	89.2	1216	2	US-10-209-787-514	Sequence 514, App
C 141	33	89.2	506	5	US-10-027-632-173566	Sequence 173566,	214	33	89.2	1216	2	US-10-261-185-513	Sequence 513, App
C 142	33	89.2	506	5	US-10-027-632-173567	Sequence 173567,	215	33	89.2	1216	2	US-10-261-185-514	Sequence 514, App
C 143	33	89.2	506	5	US-10-027-632-173567	Sequence 173567,	216	33	89.2	1216	2	US-10-681-074-513	Sequence 513, App
C 144	33	89.2	506	5	US-10-027-632-173567	Sequence 173567,	217	33	89.2	1216	2	US-10-681-074-514	Sequence 514, App
C 145	33	89.2	506	5	US-10-027-632-152361	Sequence 152361,	218	33	89.2	1216	2	US-10-425-114-7168	Sequence 7168, App
C 146	33	89.2	506	5	US-10-027-632-152362	Sequence 152362,	219	33	89.2	1216	2	US-10-425-115-164313	Sequence 164313, A
C 147	33	89.2	506	5	US-10-027-632-152361	Sequence 152361,	220	33	89.2	1216	2	US-10-425-115-25602	Sequence 25602, A

Result No.	Score	Query Match	Length	DB	ID	Description
1	34	91.9	892	3	US-09-533-559-532	Sequence 532, App
2	34	91.9	14780	3	US-09-949-016-15236	Sequence 15236, A
C	33	89.2	601	3	US-09-949-016-44638	Sequence 44638, A
C	33	89.2	601	3	US-09-949-016-76098	Sequence 76098, A
4	33	89.2	601	3	US-09-949-016-184545	Sequence 184545, A
5	33	89.2	601	3	US-09-949-016-184546	Sequence 184546, A
6	33	89.2	601	3	US-09-543-681A-739	Sequence 739, App
7	33	89.2	1116	3	US-08-838-151A-62	Sequence 62, Appl
8	33	89.2	1216	3	US-08-838-151A-62	Sequence 62, Appl

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM protein - nucleic search, using frame_plus_p2n model
Run on: October 12, 2006, 20:44:55 ; Search time 3112 Seconds
(without alignments)
188.674 Million cell updates/sec

Title: US-10-537-648-1
Perfect score: 37
Sequence: 1 YLTQPS 7

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlh
-O=/abs/ABSWEB_spool/US10537648/runat_12102006_151428_15082/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=1000
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=100 -MODE=LOCAL
-OUTFMT=plo -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs03h
-USER=US10537648 @CGN 1_1_6323 @runat_12102006_151428_15082 -NCPU=6 -ICPU=3
-NO_WMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*

1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_est7:*
7: gb_est8:*
8: gb_est9:*
9: gb_est10:*
10: gb_est11:*
11: gb_est12:*
12: gb_est13:*
13: gb_est14:*
14: gb_est15:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES				
Result	No.	Score	Query Match Length DB ID	Description
c	1	37	100.0	288 7 BB358863
	2	37	100.0	304 6 AK200728
	3	37	100.0	320 12 CB853641
	4	37	100.0	331 11 A2240574

GenCore version 5.1.9
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 12, 2006, 20:36:29 ; Search time 430 Seconds

(without alignments)

170.253 Million cell updates/sec

Title: US-10-537-648-1

Perfect score: 37

Sequence: 1 VLTQPS 7

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5

Ygapop 10.0, Ygapext 0.5

Fgapop 6.0, Fgapext 7.0

Delop 6.0, Delext 7.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Command line parameters:

-MODEL=frame_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US10537648/runat_12102006_151421_15024/app_query.fasta.1
-DB=N Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1000
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=100 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs03h
-USER=US10537648@CGN11761@runat_12102006_151421_15024 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPEXT=6 -FGAPEXT=7
-XGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N Geneseq 8:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

14: Geneseqn2005s:*

15: Geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	100.0	21	12	ADQ16436
2	37	100.0	2000	8	ADA73402
3	35	94.6	686	4	AAK57664

35	94.6	16098	8	ACC48787	Acc48787 Human Evi
35	94.6	147300	12	ADP45593	ADP45593 Human Rho
35	94.6	147700	14	ADX98570	Adx98570 Human Gua
35	94.6	147700	15	AEE96613	Aee96613 KIAA0861
34	91.9	376	6	ABN19259	Abn19259 Human ORF
34	91.9	866	4	AAH34154	Aah34154 Human col
34	91.9	892	3	AAF08009	Aaf08009 Fusarium
34	91.9	892	13	ADU52050	Adu52050 Fusarium
34	91.9	892	14	ADZ90053	Adz90053 Fusarium
34	91.9	1026	13	ADR64766	Adr64766 Cotton cd
34	91.9	1354	6	ABK35925	Abk35925 cDNA sequ
34	91.9	2000	6	ABZ16565	Abz16565 Arabidops
34	91.9	2000	8	ADA68927	Ada68927 Arabidops
34	91.9	2448	6	ABN79854	Abn79854 Fungal ZB
34	91.9	3953	13	ADT14953	Adt14953 Plant CDN
34	91.9	5379	6	ABL32330	AbL32330 Human imm
34	91.9	5837	13	ABD33270	ABD33270 Murine ca
34	91.9	128963	12	ADQ97110	Adq97110 Human can
34	91.9	242496	14	AED76150	Acn44068 Mouse CA
34	91.9	295096	11	ACN44068	Acn44068 Mouse gen
34	89.2	121	10	ADH92944	Adh92944 Human gen
33	89.2	392	5	AAH81562	Aah81562 Human dif
33	89.2	411	13	ACF86753	Acf86753 Human SIR
33	89.2	492	13	ACF81501	Acf81501 Human SIR
33	89.2	584	10	ADK52858	Adk52858 Plant DNA
33	89.2	996	13	ADS46361	AdS46361 Bacterial
33	89.2	1116	10	ADF00454	Adf00454 Bacterial
33	89.2	1216	2	AAT93320	Aat93320 Tomato-in
33	89.2	1333	10	ADC85804	Adc85804 Human GPC
33	89.2	1539	6	AAH48581	AaH48581 A thalian
33	89.2	1943	5	AAK54523	Aak54523 cDNA enco
33	89.2	2178	9	ADB08415	AdB08415 Alloiococ
33	89.2	2178	9	ADB08417	AdB08417 Alloiococ
33	89.2	2178	9	ADB08413	AdB08413 Alloiococ
33	89.2	2569	10	ADC30261	Adc30261 Human nov
33	89.2	2659	9	AAT43745	Abc43745 Molecule
33	89.2	3324	6	AAK94913	AaK94913 Human DNA
33	89.2	3999	4	AAK28025	Aax28025 Human IKA
33	89.2	3999	4	AAF29756	Aaf29756 Human IKA
33	89.2	4417	13	ADR07102	Adr07102 Full leng
33	89.2	4779	4	ABL17932	AbL17932 Drosophill
33	89.2	4788	4	AAH14533	AaH14533 Human con
33	89.2	4803	5	AAH81767	Aah81767 Human dif
33	89.2	4803	6	AAH44190	AaH44190 Human I-k
33	89.2	5924	6	ABQ80570	Abq80570 Mutant hu
33	89.2	5924	6	ABQ80569	Abq80569 Human IKB
33	89.2	5924	8	ACD13384	AcD13384 Human DNA
33	89.2	6699	6	AAK63320	AaK63320 Chemcall
33	89.2	7282	4	AAK86318	AaK86318 Human imm
33	89.2	7599	2	AAK58802	AaK58802 Human leu
33	89.2	8436	13	ADR84202	Adr84202 Aspergill
33	89.2	18888	4	ABL23020	AbL23020 Drosophill
33	89.2	20689	4	AAK78366	AaK78366 Human imm
33	89.2	32185	11	ACN4604	Acn4604 Mouse gen
33	89.2	39325	4	AAK81660	AaK81660 Human imm
33	89.2	50460	11	ACN44936	Acn44936 Mouse gen
33	89.2	54732	13	ABD33335	Abd33335 Human Can
33	89.2	56153	4	AAK46793	AaK46793 Tumour su
33	89.2	58922	13	ABD33407	Abd33407 Human can
33	89.2	86431	6	ABQ74964	AbQ74964
33	89.2	96988	3	AAF22290	Aaf22290 BAC conta
33	89.2	110000	9	ABA90521	AbA90521
33	89.2	110000	6	ABJ12064	AbJ12064
33	89.2	126990	12	ADL13332	AdL13332
33	89.2	193672	10	ADL13570	AdL13570
33	89.2	194534	12	ADQ97481	AdQ97481 Human can
33	89.2	216215	10	ADF69167	AdF69167 Human MP5
33	89.2	217409	11	ACN45150	Acn45150 Human gen
32	86.5	31	2	AAV59931	Aav59931 PCR prime
32	86.5	31	2	AAV58465	Aav58465 Primer fo
32	86.5	31	8	ABX79070	Abx79070 Human ret
32	86.5	121	4	ABA77667	Aba77667 Retinobla

C	77	32	86.5	121	4	ABA77668	Abat7668 Retinobla	150	32	86.5	3555	2	AAV58440	AAV58440 Modified
	78	32	86.5	398	13	ADK12593	Adk12593 Plant ful	151	32	86.5	3765	11	ADM01807	Adm01807 Human CDN
	79	32	86.5	466	4	ABL09413	Ab109413 Drosophil	152	32	86.5	3765	11	AEC84737	Aec84737 Human CDN
C	80	32	86.5	576	12	ADO34573	Ado34573 Human SLI	C	153	3877	12	ADP90661	Adp90661 Mouse ext	
	81	32	86.5	591	13	ACN60693	Acn60693 Cotton gy	154	32	86.5	4432	13	ADV40792	Adv40792 Rat cardi
C	82	32	86.5	600	10	ACF68049	Acf68049 Photorhab	155	32	86.5	4579	1	AAN81261	Aan81261 Probe for
C	83	32	86.5	631	5	ABV50016	Abv50016 Human pro	156	32	86.5	4597	1	AAN81369	Aan81369 Human ret
C	84	32	86.5	639	10	ADF00608	Adf00608 Bacterial	157	32	86.5	4597	2	AAQ70536	Aaq70536 Human ret
C	85	32	86.5	795	6	AB212201	Ab212201 Arabidops	158	32	86.5	4597	2	AAQ70536	Aaq70536 Human ret
C	86	32	86.5	1020	10	ADC92233	Adc92233 E. faeciu	159	32	86.5	4600	13	ADR52909	Adr52909 Drug ther
	87	32	86.5	1024	10	ABZ83423	Abz83423 Toxicolog	160	32	86.5	4641	4	ABL16126	Ab116126 Drosophil
	88	32	86.5	1056	3	AAZ847383	Aaz847383 Arabidops	161	32	86.5	4740	6	ABK86079	Abk86079 Human ret
	89	32	86.5	1063	3	AAZ847383	Aaz847383 Arabidops	162	32	86.5	4740	10	ADE84952	Ad84952 Farnesyl
C	90	32	86.5	1125	8	ACA332019	Ac332019 Prokaryot	163	32	86.5	4740	10	ADP67029	Adp67029 Gene #119
C	91	32	86.5	1161	6	ABL89390	Ab189390 Babesia m	164	32	86.5	4740	12	ADP21395	Adp21395 Gene Rb1
C	92	32	86.5	1161	10	ADE06059	Ad06059 BMNI-rela	165	32	86.5	4740	14	ADV15003	Adv15003 DNA encod
C	93	32	86.5	1162	6	ABL89383	Ab189383 Babesia m	166	32	86.5	4740	14	ADY19476	Ady19476 DNA encod
C	94	32	86.5	1162	10	ADE06052	Ad06052 BMNI-rela	167	32	86.5	4740	15	AEF74797	Aef74797 Human pol
C	95	32	86.5	1248	6	ABL89429	Ab189429 Babesia m	168	32	86.5	4741	12	ACF57516	Acf57516 Human Rb
C	96	32	86.5	1248	6	ABL89429	Ab189429 Babesia m	169	32	86.5	4839	3	AAZ88444	Aaz88444 Human and
C	97	32	86.5	1304	13	ADT15452	Adt15452 Plant CDN	170	32	86.5	4839	3	AAZ88444	Aaz88444 Human and
C	98	32	86.5	1775	11	ADP65595	Adp65595 Human alp	171	32	86.5	4839	6	ABL62873	Ab162873 Breast ca
C	99	32	86.5	1904	13	ADT18553	Adt18553 Plant CDN	172	32	86.5	4839	12	ADP72311	Adp72311 Human Rb
C	100	32	86.5	1974	8	ACA53600	Ac53600 Prokaryot	173	32	86.5	4839	12	ADP72311	Adp72311 Human Rb
	101	32	86.5	2263	14	AEA22558	Aea22558 Mouse LRM	174	32	86.5	4839	15	AEF74994	Aef74994 Human pol
	102	32	86.5	2466	4	ABL09412	Ab109412 Drosophil	175	32	86.5	5056	1	AAN90489	Aan90489 CDNA of h
	103	32	86.5	2787	14	AEC21879	Aec21879 Human ret	176	32	86.5	5430	4	AAS46291	Aas46291 Tumour su
	104	32	86.5	2824	14	ABE55609	Ab555609 Human ret	177	32	86.5	5884	6	ABL34164	Ab134164 Human imm
	105	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	178	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	106	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	179	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	107	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	180	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	108	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	181	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	109	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	182	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	110	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	183	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	111	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	184	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	112	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	185	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	113	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	186	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	114	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	187	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	115	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	188	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	116	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	189	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	117	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	190	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	118	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	191	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	119	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	192	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	120	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	193	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	121	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	194	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	122	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	195	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	123	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	196	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	124	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	197	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	125	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	198	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	126	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	199	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	127	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	200	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	128	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	201	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	129	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	202	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	130	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	203	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	131	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	204	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	132	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	205	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	133	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	206	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	134	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	207	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	135	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	208	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	136	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	209	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	137	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	210	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	138	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	211	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	139	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	212	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	140	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	213	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	141	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	214	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	142	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	215	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	143	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	216	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	144	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	217	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	145	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	218	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	146	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	219	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	147	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	220	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	148	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	221	32	86.5	6301	6	ABL34164	Ab134164 Human imm
	149	32	86.5	2994	2	AAQ04713	Aaq04713 Cancer su	222	32	86.5	6301	6	ABL34164	Ab134164 Human imm